

STIC-Biotech/ChemLib

86436

From: McElwain, Elizabeth
Sent: Tuesday, February 11, 2003 10:48 AM
To: STIC-Biotech/ChemLib
Subject: sequence search

Please search for prior art and for interference:

09/883,797 - for DNA encoding SEQ ID NO: 2.

Thank you,
Beth

Elizabeth F. McElwain, Ph.D.
U.S. Patent and Trademark Office
Tech Center 1600, Art Unit 1638
room CM1-9E11
mailbox CM1-9E12
703-308-1794
elizabeth.mcelwain@uspto.gov

Point of Contact:
Toby Port
Technical Info. Specialist
CM1 6A04
703-308-3534

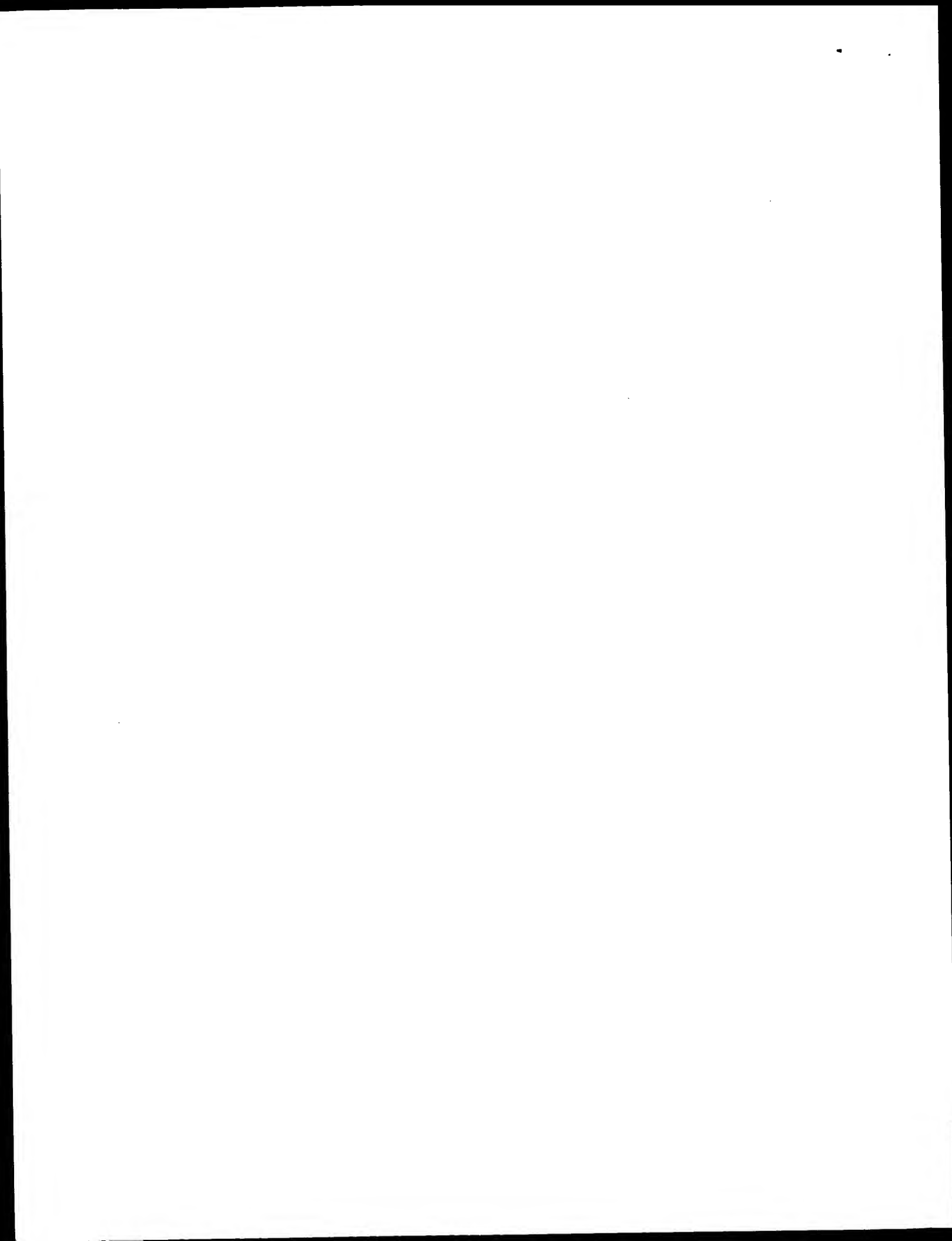
Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 2/14
Date Completed: 2/20
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____



GenCore version 5.1.4.p5.4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 08:33:57 ; Search time 3473 Seconds
(without alignments)
4357.460 Million cell updates/sec

Title: US-09-883-797-2

Perfect score: 2680

Sequence: 1 MDRRLTAEMAFRDSSSAVI.....EMTGNWAGSTIDQYPKVKVQ 520

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2.1/USPTO.spool/US09883797/runat_14022003_102501_19502/app_query.fasta_1.711
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*

29: em.vi.*
30: em.htg.hum.*
31: em.htg.inv.*
32: em.htg.other.*
33: em.htg.mus.*
34: em.htg.pln.*
35: em.htg.rod.*
36: em.htg.mam.*
37: em.htg.vrt.*
38: em.sy.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2680	100.0	1560	6	AR174886 Sequence
2	2680	100.0	1563	6	AX412586 Sequence
3	2680	100.0	1563	8	AF053345 Arabidops
4	2680	100.0	1618	8	AY096568 Arabidops
5	2680	100.0	1896	8	AY074285 Arabidops
6	2680	100.0	86436	8	AC007323 Genomic s
7	2020.5	75.4	127990	8	AF004939 Lotus jap
8	1764	65.8	1929	8	AF082033 Hemerocal
9	1720.5	64.2	131142	8	AC129008 Genomic s
10	1679	62.6	139914	2	AP003623 Oryza sat
11	1674.5	62.5	119028	2	AC098832 Oryza sat
12	1658	61.9	2018	8	ZMA292770 Zea mays
13	1639	61.2	95167	8	AC003105 Arabidops
14	1626	60.7	1803	8	AF424620 Arabidops
15	1626	60.7	1845	8	AY035030 Arabidops
16	1608	60.0	1807	8	AF247134 Limnanthe
17	1595.5	59.5	2143	6	AX155071 Sequence
18	1584	59.1	203125	2	AC120986 Oryza sat
19	1581.5	59.0	1662	8	AY074518 Arabidops
20	1574	58.7	144359	8	AC087723 Oryza sat
21	1563	58.3	1548	6	AR174892 Sequence
22	1563	58.3	120977	8	AC025808 Genomic s
23	1559.5	58.2	178025	2	AP005008 Oryza sat
24	1531.5	57.1	1611	6	AR174890 Sequence
25	1531.5	57.1	114418	8	AC007047 Arabidops
26	1525.5	56.9	1765	8	AY082610 Tropaeolu
27	1521.5	56.8	1812	8	SCU37088 Simmondsia
28	1519.5	56.7	1783	6	I14085 Sequence 11
29	1519.5	56.7	1783	6	I14085 Sequence 3
30	1513.5	56.5	1819	8	AY089012 Arabidops
31	1505	56.2	5600	8	AF188485 Arabidops
32	1505	56.2	55870	8	AC005819 Arabidops
33	1497	55.9	1733	6	I14084 Sequence 10
34	1497	55.9	1733	6	I70545 Sequence 2
35	1472	54.9	1903	8	AY072823 Gossypium
36	1468.5	54.8	87937	8	ATAC009400 Arabidops
37	1443.5	53.9	87286	6	AB026651 Arabidops
38	1441	53.8	1650	6	AR174889 Sequence
39	1438.5	53.7	1491	6	AR165358 Sequence
40	1438.5	53.7	1502	6	AR174891 Sequence
41	1438.5	53.7	1807	6	AR165357 Sequence
42	1438.5	53.7	1827	8	AY087518 Arabidops
43	1438.5	53.7	1829	8	AF129511 Arabidops
44	1438.5	53.7	3722	6	AR165356 Sequence
45	1438	53.7	1911	8	AY039563 Arabidops

ALIGNMENTS

RESULT 1

AR174886
LOCUS AR174886 1560 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 1 from patent US 6307128.
ACCESSION AR174886
VERSION AR174886.1 GI:17915206
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1560)
AUTHORS Jaworski, J.G., Post-Beittenmiller, M. Ann. and Todd, J.
TITLE Fatty acid elongases
JOURNAL Patent: US 6307128-A 1 23-Oct-2001;
FEATURES Location/Qualifiers
source 1..1560
/organism="unknown"
BASE COUNT 420 a 355 c 378 g 407 t
ORIGIN

Alignment Scores:
Pred. No.: 2,1e-240 Length: 1560
Score: 2680.00 Matches: 520
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-883-797-2 (1-520) x AR174886 (1-1560)

Qy 1 MetAspArgGluArgLeuThrAlaGluMetAlaPheArgAspSerSerAlaValIle 20
Db 1 ATGGATCAGAGAGATTAAACGGCGGAGATGGCGTTTCGAGATTATCATCATCGCGGTATA 60
Qy 21 ArgIleArgArgLeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeu 40
Db 61 AGAATTCGAAGACGTTTGCCTGCGGATTATTAACTGCTTAAAGCTCAATACGTGAAGCTT 120
Qy 41 GlyLeuHisAsnSerCysAsnValThrThrIleLeuPhePheLeuIleLeuProLeu 60
Db 121 GGACTTCAACAACCTGTCACGTCAGCCACCATCTCTCTTCTTAATTATCTCTCTTAA 180
Qy 61 ThrGlyThrValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrp 80
Db 181 ACCGGAACCGTGCTGCTTCAAGTAAACCGGCTTAAACGTTTCGATACGTTCTCTGAGCTTGG 240
Qy 81 SerAsnGlnAlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSer 100
Db 241 TCTAACACGCGGTTCAACTCGACACGCGGACGAGACTTACCTGCTTGGTTTCTCTCTCC 300
Qy 101 PheValLeuThrLeuTyrValAlaAsnArgSerLysProValTyrLeuValAspPheSer 120
Db 301 TTCGTTTGGACCTCTACCTGCTTAAACCGGCTTAAACCGGTTTACCTAGTGGATTCTCC 360
Qy 121 CysTyrLysProGluAspGluArgLysIleSerValAspSerPheLeuThrMetThrGlu 140
Db 361 TGCCTAAACCGGAGACGAGCGGCTAAATATCATAGATTCGTTCTTTCGATGACTGAG 420
Qy 141 GluAsnGlySerPheThrAspAspThrValGlnPheGlnGlnArgIleSerAsnArgAla 160
Db 421 GAAATGGATCATTCACCGATGACAGGTTTCAGTTCAGCAAGAAATCTCGAACCGGGCC 480
Qy 161 GlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProProLysLeuAsn 180
Db 481 GGTTCGGAGACGAGACGATATCGCCACGTCGTCGATTAACCTCAACCGCCCGGAAAGCTAAAT 540
Qy 181 MetSerGluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPhe 200
Db 541 ATGTACAGAGCAGCTGCCAAGCTGAAGCGGTTATGTTTGGAGCCTTAGATTCCTCTTC 600
Qy 201 GluLysThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPhe 220
Db 601 GAGAAACCGGAATTAAACCGCGCGGAGTCGGAATCTTGATAGTAAACTGCAGCTTATTC 660

Qy 221 AsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIle 240
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Qy 241 LysSerTyrAsnLeuGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAla 260
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Qy 261 AsnAsnLeuLysAlaAsnProAsnSerTyrAlaValValValSerThrGluAsnIle 280
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Qy 281 ThrLeuAsnTrpTyrPheGlyAsnArgSerMetLeuLeuCysAsnCysIlePheArg 300
Db 841 ACCCTAACTGGTACTTCGGAATGACCGGTCAATGCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Qy 301 MetGlyGlyAlaIleLeuLeuSerAsnArgArgGlnAspArgLysSerLysTyr 320
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Qy 321 SerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysVal 340
Db 961 TCCTGGTCAACGCTCGTTCGAACACATAAAGGATCAGACGACAAAGAACTACAATTCGCTG 1020
Qy 341 TyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSer 360
Db 1021 TACCAGAAAGGAGACGAGAGAGGAACTCGTCTCTCTTTAGCTAGAGCGTCAATGCT 1080
Qy 361 ValAlaGlyAspAlaLeuLysThrAsnIleThrLeuGlyProMetValLeuProLeu 380
Db 1081 GTCCCGGAGCGCTCTGAAACAAACATCACGACTTATGAGCCGATGGTCTTCCATTTG 1140
Qy 381 SerGluGlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysVal 400
Db 1141 TCAGAGCAGTGTATGTTCTTCTGATTTCTTGTGCTCAAAAGAAAGATGTTCAAGTTAAAGTT 1200
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Db 1261 AGACCGTCTAGACGAGTGCAGAAAGATCTTGATCTCAAAAGATTGGCACATGGAACCT 1320
Qy 441 SerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTrpTrpGluMet 460
Db 1321 TCTAGAATGACTTTCACAGATTTTGGTAACACTTCGAGTAGCTCGCTTTGGTATGAGATG 1380
Qy 461 AlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPhe 480
Db 1381 GCTTATACCGAAGCTAAGGGTCGGGTTAAAGCTGCTGACCGACTTGGCAGATTGGCTTT 1440
Qy 481 GlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGlu 500
Db 1441 GGATCGGTTTCAAGTGAATAGTCGGGTTTGGAAAGCCTTACGACCGGTTTCGACGGAG 1500
Qy 501 GluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysValGln 520
Db 1501 GAGATGACCGGTAATGCTTGGCTGCTTGGCTGCTTGGCTGCTTGGCTGCTTGGCTGCTTGGCT 1560

RESULT 2
AX412586 1563 bp DNA linear PAT 14-JUN-2002
LOCUS AX412586
DEFINITION Sequence 350 from Patent WO0222675.
ACCESSION AX412586
VERSION AX412586.1 GI:21445044
KEYWORDS thale cress.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1

AUTHORS

Glazebrook, J., Wang, X., Dangl, J.L., Eulgem, T. and Zhu, T.
 TITLE plant genes, the expression of which are altered by pathogen infection

JOURNAL

Patent: WO 0222675-A 350 21-MAR-2002;
 Syngenta Participations AG (CH); UNIVERSITY OF NORTH CAROLINA AT
 CHAPEL HILL (US); Glazebrook, Jan (US); Wang, Xun (US); Dangl,
 Jeffrey L. (US); Eulgem, Thomas (US)

FEATURES

Location/Qualifiers

1..1563

/organism="Arabidopsis thaliana"

/db_xref="taxon:3702"

BASE COUNT 421 a 355 c 379 g 408 t

ORIGIN

Alignment Scores:

Pred. No.: 2..le-240 Length: 1563
 Score: 2680.00 Matches: 520
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-883-797-2 (1-520) x AX412586 (1-1563)

QY 1 MetAspArgGluArgLeuThrAlaGluMetAlaPheArgAspSerSerAlaValIle 20
 Db 1 ATGATCGAGAGAGATTAAACGGCGAGATGCGTTTCGAGATTTCATCATCGCCGTTATA 60
 QY 21 ArgIleArgArgGluProAspLeuLeuThrSerValLysLeuLysTyrValLysLeu 40
 Db 61 AGAATTCGAAGACGTTTCCGCGGATTATTAACGTCGCTTAAGCTCAATACGTGAAGCTT 120
 QY 41 GlyLeuHisAsnSerCysAsnValThrThrIleLeuPhePheLeuIleIleLeuProLeu 60
 Db 121 GGACTTCACAACCTCTGCAACGTCGACACCATCTCTCTCTCTTAATATTCCTCCCTTA 180
 QY 61 ThrGlyThrValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrp 80
 Db 181 ACCGGAAACCGTGTGGTTCAGCTAACCGGTCCTAACGTCGATGCTCTGAGCTTTGG 240
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 QY 141 GluAsnGlySerPheThrAspThrValGlnPheGlnArgIleSerAsnArgAla 160
 Db 421 GAAATGGATCATTCACCGATGACACGCTTACGTCAGTCCAGCAAGATCTCGAACCGGCC 480
 QY 161 GlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProProLysLeuAsn 180
 Db 481 GGTGTGGGAGACGACGCTATCTGCCACGTGGCATAAATCTCAACGCCCGCGAGCTAAAT 540
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 QY 221 AsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIle 240
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 QY 301 MetGlyGlyAlaAlaIleLeuLeuSerAsnArgArgGlnAspArgLysLysSerLysTyr 320
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 QY 321 SerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysVal 340
 Db 961 TCCTGTGTCACGCTGCTTCAACACATAAAGATCAGACGACAGCACTACATTTCCGTG 1020
 QY 341 TyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSer 360
 Db 1021 TACCAGAAGGAGACGAGAGAGAACTCGTCTCTTTAGCTAGAGAGCTCATGTCT 1080
 QY 361 ValAlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeuProLeu 380
 Db 1081 GTCCGCGGAGACGCTCTGAAAACAAACATCAGCACTTTAGCACCGATGGTTCTTCCATTTG 1140
 QY 381 SerGluLysLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysVal 400
 Db 1141 TCAGACGAGTTGATGTTCTTGTATTTCTTGTCTCAAAAGGAGATGTTCAAGTTAAAGTT 1200
 QY 401 LysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGly 420
 Db 1201 AAACCGTATATTCGCGATTTCAGCTAGCTTTGAGCATTTCTGATTCACGCGAGGAGT 1260
 QY 421 ArgAlaValLeuAspGluValGlnLysAsnLeuAspLysAspTrpHisMetGluPro 440
 Db 1261 AGAGCGGTTCTAGACGAGTGCAGAAAGATCTTGATCTCAAGATGGCATGGAACCT 1320
 QY 441 SerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTrpTyrGluMet 460
 Db 1321 TCTAGAATGACITTCACAGATTTCGACACTTCGAGTAGCTCGCTTTGGTAGAGATG 1380
 QY 461 AlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPhe 480
 Db 1381 GCTTATACGGAAGCTAAAGGTCGGGTTAAAGCTGAGTGGTACCGACTTTGGCAGATTGCGTT 1440
 QY 481 GlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGlu 500
 Db 1441 GGATCGGTTTCAAGTGTAAATAGTCGGGTTTGAAAGCGTTTACGACCGGTTTCGACGGAG 1500
 QY 501 GluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysValGln 520
 Db 1501 GAGATGACCGGTAATGCTTGGGCTGTTGATTCATATATCCGGTTAAAGTTGTGCAA 1560

RESULT 3

AF053345

LOCUS

DEFINITION

(KCS1) gene, complete cds.

ACCESSION

AF053345

VERSION

AF053345.1

GI:4091809

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana.

Arabidopsis thaliana

Eukaryota; Viridiplantae;

Spermatophyta; Magnoliophyta;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 1563)

Todd, J... Post-Beittemiller, D. and Jaworski, J.G.

KCS1 encodes a fatty acid elongase 3-ketoacyl-CoA synthase

affecting wax biosynthesis in Arabidopsis thaliana

Plant J. 17 (2), 119-130 (1999)

Qy 501 GluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysValValGln 520
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 Db 1501 GAGATACCGGTAATGCTTGGGCTGGTTCGATTGATCAATATCCGGTTAAAGTTGTGCAA 1560

RESULT 4
 AY096568 1618 bp mRNA linear PUN 06-MAY-2002
 LOCUS
 DEFINITION Arabidopsis thaliana putative fatty acid elongase 3-ketoacyl-CoA
 synthase 1 (At1g01120) mRNA, complete cds.
 AY096568
 VERSION Arabidopsis thaliana
 KEYWORDS F1I_CDNA.
 SOURCE Arabidopsis thaliana
 ORGANISM Arabidopsis thaliana

REFERENCE
 AUTHORS
 Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,
 Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,
 Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
 Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
 Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
 Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
 Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,
 Shinozaki, K., Davis, R.W., Ecker, J.R., and Theologis, A.,
 Arabidopsis Open Reading Frame (ORF) Clones
 Unpublished

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,
 Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,
 Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
 Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
 Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
 Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
 Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,
 Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
 Direct Submission
 Submitted (16-APR-2002) Plant Gene Expression Center, 800 Buchanan
 Street, Albany, CA 94710, USA
 The RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL cDNAs (RAFL cDNA : "RIKEN
 Arabidopsis Full-Length cDNA"): Seki, M., Narusaka, M., Ishida, J.,
 Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
 Hayashizaki, Y. and Shinozaki, K.

TITLE
 JOURNAL
 COMMENT
 The Salk, Stanford, PGEC (SSP) Consortium members constructed and
 sequenced the PUNI (ORF) clones using the RAFL cDNAs: Yamada, K.,
 Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M.,
 Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C.,
 Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H.,
 Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J.,
 Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P.,
 Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.

FEATURES
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 Best Local Similarity: 100.00% Mismatches: 0
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 DB: 8 Gaps: 0
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DEFINITION	synthase I (Atlg01120) mRNA, complete cds.			
ACCESSION	AY074285			
VERSION	AY074285.1	GI:18377663		
KEYWORDS	FLI_CDNA.			
SOURCE	Arabidopsis thaliana.			
ORGANISM	Arabidopsis thaliana.			
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	Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
1 (bases 1 to 1896)	Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chang,E., Dale,J.M.,			
Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chang,E., Dale,J.M.,	Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,			
Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,	Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Kim,C.,			
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,	Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,			
Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,	Davis,R.W., Ecker,J.R. and Theologis,A.			
Arabisopsis Full Length cDNA Clones				
2 (bases 1 to 1896)	Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,			
Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,	Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,			
Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,	Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,			
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Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,	Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.			
Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.				
Direct Submission				
Submitted (11-JAN-2002)	Plant Gene Expression Center, 800 Buchanan			
Street, Albany, CA 94710, USA				
RIKEN Genomic Sciences Center (GSC) members carried out the				
collection and clustering of RAPL cDNAs (RAPL cDNA: 'RIKEN				
Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,				
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,				
Hayashizaki,Y. and Shinozaki,K.				
The Salk, Stanford, PGE (SSP) Consortium members carried out the				
sequencing and annotation of the RAPL cDNAs: Yamada,K., Banh,J.,				
Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M.,				
Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C.,				
Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H.,				
Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J.,				
Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P.,				
Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.				
Yamada,K. (SSP/PGE) and Seki,M. (RIKEN GSC) contributed equally to				
this work. Shinozaki,K. (RIKEN GSC) and theologis,A. (SSP/PGE)				
contributed equally to this work as PIs.				
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Query Match:	100.00%	Indels:	0
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US-09-883-797-2 (1-520) x AY074285 (1-1896)

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QY	221	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	His	Tyr	Lys	Met	Arg	Glu	Asp	240
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RESULT 6
AC007323/C

LOCUS	AC007323	86436 bp	DNA	linear	PLN 19-JAN-2000
DEFINITION	Genomic sequence for <i>Arabidopsis thaliana</i> BAC T25K16 from chromosome I complete sequence.				

ACCESSION AC007323
VERSION AC007323.5 GI:6587720

KEYWORDS

SOURCE *Arabidopsis thaliana*.

ORGANISM

Eukaryota; Viridiplan

REFERENCE

REFERENCE

EVOLUTORY

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

1

REFERENCE AUTHORS TITLE JOURNAL	Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA 3 (bases 1 to 86436) Ecker, J.R. Direct Submission Submitted (11-AUG-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA 4 (bases 1 to 86436)	CDS	RPMSLVQAHOFGNFGNFENFPTTSQYNSRHPPLPEYNVPIHRLGNIGNHORSYNT ORQFEYGYGNLAGCYTCSPLDHRNIVGSEPLVIDSVVPVPLPMLPLPP PSTAGKRRLFLGVNMEGNDYNQOEKSWLVRGETGASSSSSSALRLNLSTDDDDND DGGDDDDQFAKKGSLSLNFNP join(23221..24174,24244..24357,24412..24664,24743..25137, 25226..25445,25527..25711,25783..25905,25994..26478, 26564..26730,26814..26983,27074..27235,27320..27415, 27505..28133,28314..28507,28592..28782,28862..30013, 30112..30518,30604..30781) /note= "similar to UFDI protein embi CAB10321.1; similar to ESTs gb H36434, gb A1996152.1" /codon_start=1 /evidence=not_experimental /product="T25K16.4" /protein_id="AAF26461.1" /db_xref="GI:6715634"
REFERENCE AUTHORS TITLE JOURNAL	Chao, Q., Brooks, S., Buehler, E., Johnson-Hopson, C., Khan, S., Kim, C., Shinn, P., Altairi, H., Bei, B., Chin, C., Chlou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukhar, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J. Direct Submission Submitted (19-JAN-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA On Dec 16, 1999 this sequence version replaced gi:5729683. Location/Qualifiers 1..86436 /organism="Arabidopsis thaliana" /db_xref="taxon:3702" /chromosome="1" /clone="T25K16" join(3462..3615,3698..3978,4077..4307,4408..4797, 4876..5028,5141..5332) /note= "containing similarity to NAM-like proteins gi 3695378" /codon_start=1 /evidence=not_experimental /product="T25K16.1" /protein_id="AAF26460.1" /db_xref="GI:6715633"	CDS	complement(join(31084..31126,31223..31304,31341..31515, 31635..31700,31790..31897,31984..32049,32133..32161, 32249..32372)) /note= "putative inorganic pyrophosphatase gi 3510259; similar to ESTs gb A42316, gb A1994042.1, gb A1994013.1, emb Z29202" /codon_start=1 /evidence=not_experimental /product="T25K16.5" /protein_id="AAF26475.1" /db_xref="GI:6715648"
REFERENCE AUTHORS TITLE JOURNAL	Chao, Q., Brooks, S., Buehler, E., Johnson-Hopson, C., Khan, S., Kim, C., Shinn, P., Altairi, H., Bei, B., Chin, C., Chlou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukhar, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J. Direct Submission Submitted (19-JAN-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA On Dec 16, 1999 this sequence version replaced gi:5729683. Location/Qualifiers 1..86436 /organism="Arabidopsis thaliana" /db_xref="taxon:3702" /chromosome="1" /clone="T25K16" join(3462..3615,3698..3978,4077..4307,4408..4797, 4876..5028,5141..5332) /note= "containing similarity to NAM-like proteins gi 3695378" /codon_start=1 /evidence=not_experimental /product="T25K16.1" /protein_id="AAF26460.1" /db_xref="GI:6715633"	CDS	complement(join(6617..6953,7266..7351,7464..7603, 7916..7998,8087..8166,8273..8368)) /note= "hypothetical protein" /codon_start=1 /evidence=not_experimental /product="T25K16.2" /protein_id="AAF26477.1" /db_xref="GI:6715650"
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US-09-883-797-2 (1-520) x AC007323 (1-86436)

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Db 57276 GCTTATACCGAAGCTAAGGGTCGGGTAAAGCTGGTACCACCTTTTGCAGATTGCGTTT 57217

QY 481 GlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGlu 500
Db 57216 GGATCGGTTCAAGTGTAAATAGTCGGTTTGGAAAGCGTTTACACCGGTTTCGACGAG 57157

QY 501 GluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysValGln 520
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RESULT 7

AP004939/c

LOCUS

DEFINITION

Lotus japonicus genomic DNA, chromosome 1, clone: Lj17M09, TM0105,
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complete sequence.

ACCESSION AP004939

VERSION AP004939.1 GI:21907955

KEYWORDS HTG.

SOURCE Lotus japonicus DNA, clone_lib:LjT library clone:LjT17M09.

ORGANISM

Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
Lotus.

REFERENCE

1 Kaneko, T., Nakamura, Y., Asamizu, E., Kato, T., Sato, S. and Tabata, S.
Structural Analysis of a Lotus japonicus Genome. I. Sequence
Features and Mapping of Sixty-six TAC clones which cover the 6.7 Mb
Regions of the Genome

JOURNAL

REFERENCE Unpublished

TITLES 2 (bases 1 to 127990)

AUTHORS

Nakamura, Y.

JOURNAL

Direct Submission
Submitted (26-MAR-2002) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail: ynekazusa.or.jp,
URL: http://www.kazusa.or.jp, Tel: 81-438-52-3935,
Fax: 81-438-52-3934)

FEATURES

source

Location/Qualifiers

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US-09-883-797-2 (1-520) x AP004939 (1-127990)

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LOCUS
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VERSION
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KEYWORDS
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  1 (bases 1 to 1929)
  Panavas, T., Pikula, A., Reid, P.D., Rubinstein, B. and Walker, E.L.
  Identification of senescence-associated genes from daylily petals
  Plant Mol. Biol. 40 (2), 237-248 (1999)
  99339248
  PUBMED
  10412903
REFERENCE
  2 (bases 1 to 1929)
  Panavas, T., Pikula, A., Reid, P.D., Rubinstein, B. and Walker, E.L.
  Direct Submission
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US-09-883-797-2 (1-520) x AF082033 (1-1929)

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Qy 21 ArgIleArgArgLeuProAspLeuThrSerValIleLeuLeuLeuLeuLeuLeuLeuLeu 40
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us-09-883-797-2.p2n.rge

/chromosome="3"
/clone="OSJNB0096114"
/clone_lib="ECORI"

BASE COUNT 35707 a 30896 c 29581 g 34958 t
ORIGIN

Alignment Scores: 3.38e-148 Length: 131142
Pred. No.: 1720.50 Matches: 338
Score: 76.52% Conservative: 76
Percent Similarity: 62.48% Mismatches: 86
Best Local Similarity: 64.20% Indels: 41
Query Match: 8 Gaps: 8
DB:

US-09-883-797-2 (1-520) x AC129008 (1-131142)

QY 1 MetAspArgGluArgLeuThrAlaGluMetAlaPheArgAspSerSer----- 16
DB 56991 ATGGAGCGGAGCGGCTACGGCGGAGATGGCTTCGGCGAGCGAGCGCGCGCGCGCGCGG 57050
QY 17 -----SerAlaValIleArgIleArgArgLeuProAspLeuThr 31
DB 57051 GGGAGTGGCGCGGAGCATCTGTATCAAGATCGGCGCGCGCTCCCGACTTCGCGCGG 57110
QY 32 SerValLysLeuLysTyrValLysLeuGlyLeuHisAsnSerCysAsnValThrThrle 51
DB 57111 TCCGTGAACCTCAAGTACGTCAAGCTCGGATCGGCGAGCGCGCGCGCGCTCACGTCG 57167
QY 52 LeuPhePheLeuIleLeuProLeuThrGlyThrValLeuValGlnLeuThrGlyLeu 71
DB 57168 -----TACCTGCCCATGCTGTGCGTGGCGTGTCTCGCGCTCCGCGCGCTAC 57212
QY 72 ThrPheAspThrPheSerGluLeuTrpSerAsnGlnAlaValGlnLeuAspThrAlaThr 91
DB 57213 TCCTTC-----GTCCGCTCGACGTCACTCATCTAC 57239
QY 92 Arg-----LeuThrCysLeuValPheLeuSer-----PheValLeuThr 104
DB 57240 CGGTCCATCGACCTGCTCACCTGCTGCGCTGGCGCGCGCGCTGCTGCTGCTCACC 57299
QY 105 LeuThrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysPro 124
DB 57300 GTCTACTTCAAGCGCGCGCGCGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 57359
QY 125 GluAspGluArgLysLysLysSerValAspSerPheLeuThrMetThrGluGluAsnGlySer 144
DB 57360 GACGACGACGACAAAGATCTCCAAGGAAGGCTTCTTCGAGATGACCGAGAGACCGGCTGC 57419
QY 145 PheThrAspAspThrValGlnPheGlnArgIleSerAsnArgAlaGlyLeuGlyAsp 164
DB 57420 TTCAATGACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 57479
QY 165 GluThrTyrLeuProArgGlyIleThrSerThrProLysLeuAsnMetSerGluAla 184
DB 57480 GAGAGTACCTCCCTCCCGCGCTCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 57539
QY 185 ArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLysThrGly 204
DB 57540 AGGATGGAGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 57599
QY 205 IleLysPro---AlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnProThr 223
DB 57600 ATCAACCCGAAACGCGAGCTGGGCACTCTCATCTGACCTGACCTGACCTGACCTGACCTG 57659
QY 224 ProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspLysSerTyr 243
DB 57660 CGCT 57719
QY 244 AsnLeuGlyGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnLeu 263
DB 57720 AACCTCGGCGGATGGGTCAGCGCGCGCTCATCGCTCATCGCTCATCGCTCATCGCTCATG 57779
QY 264 LeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsn 283

QY 396 PheLysLeuLys---ValLysProTyrIleProAspPheLysLeuAlaPheGluHisPhe 414
DB 1166 CTTAAACTGAAAGGGGTGAGCGGTACATTTCCAAATTTAAACCGCGATTGTGACACTTC 1225

QY 415 CysIleHisAlaGlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLysLys 434
DB 1226 TGGCTGCAGCTGGGCGGAGCAGCTGTTGATGAGTCTGAGAAAGATCTGGGCTTGAG 1285

QY 435 AspTrpHisMetGluProSerArgMetThrLeuHisArgPheGlyAsnThrSerSerSer 454
DB 1286 AAGACAGACATGAGGAGCATCGAAGCGTGTCCACCGGTTTGGGAACACTAGTAGCAGC 1345

QY 455 SerLeuTrpTyrGluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArg 474
DB 1346 TCCTGTGGGTATGAGCTGGCTTACAATGAGCAAGGGGAGAGTCGGAAGGGGTGATCGA 1405

QY 475 LeuTrpGlnIleAlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeu 494
DB 1406 GTTTGGCAGATTGGGTTGGGTCGGGTTCAAGTGTACAGTGCAGTGTGGAAGGCCATG 1465

QY 495 ArgProValSerThrGluGluMetThrGly-----AsnAlaTrp 507
DB 1466 AAAGACGTTCCGGCAATGATGCAACAGCTAGTGGGCTTCTCGAATGTGCAATCCGTGG 1525

QY 508 AlaGlySerIleAspGlnTyrProValLys 517
DB 1526 GGGGATTGCATTGACCGCTACCCAGTCAAG 1555

RESULT 9
AC129008 131142 bp DNA linear PLN 24-JUL-2002
LOCUS Genomic sequence for Oryza sativa, Nipponbare strain, clone
OSJNB0096114, from chromosome 3, complete sequence.

AC129008
AC129008.1 GI:21954009
HTG.
Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 131142)

McCombie, W.R., de la Bastide, M., Spiegel, L., Preston, R.,
Nascimento, L., Zutavern, T., Balija, V., Bell, M., Miller, B.,
Muller, S., Katzenberger, F., Sullivan, P., Yang, C., Dike, S.,
O'Shaughnessy, A., Palmer, L. and Dedhia, N.
Genomic sequence for Oryza sativa, Nipponbare strain, clone
OSJNB0096114, from chromosome 3, complete sequence
Unpublished

2 (bases 1 to 131142)
McCombie, W.R.
Direct Submission
Submitted (24-JUL-2002) Lita Annenberg Hazen Genome Center, Cold
Spring Harbor Laboratories, 1, Bungtown Road, Cold Spring Harbor,
NY 11724, USA

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30);
an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest.
The nucleotide sequence of this clone was generated by combining
Syngenta and Cold Spring Harbor Laboratory Genome Research Center
sequencing data. OSJNB0096114 overlaps clone OSJNB0078P24
(AC118672) from base 1 to base 9426. The overlap is from base
138843 to base 148268 on OSJNB0078P24.

Location/Qualifiers
1. 131142
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"

FEATURES
source

Thu Feb 20 11:03:33 2003

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Qy 223 ThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSer 242
Db 61535 ACGCGTGTCTGCGCCATGTTGTGAACCACTACAAAGTGAGGGGAATGTATCAGC 61594
Qy 243 TyrAsnLeuGlyGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAsp 262
Db 61595 TACAACCTCGGGGATGGGTGCGATGCGGCTTGTCTCCGTCGATCGCCAAAGGAC 61654
Qy 263 LeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeu 282
Db 61655 TTGCTCGAGTGCACCAAACTCGTACGCGCTGGTGTGACGATGGAGAACATCACGCTC 61714
Qy 283 AsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGly 302
Db 61715 AATTGTFACCTTGGCAACACCGGTCGATGCTGTCGAAATTCCTGTTCCGGATGGC 61774
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Qy 363 GlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeuProLeuSerGlu 382
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Qy 383 GlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLeuLysValLysPro 402
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Qy 423 ValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArg 442
Db 62135 GTGCTGGATGAGCTGGAGAAACATTTGGAGTTGACTGACTGGACATGGAGCATCTAGG 62194
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Qy 463 ThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySer 482
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Qy 483 GlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMet 502
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Qy 503 ThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal 518
Db 62372 GAGAACAACCCCTGGATGATGAGATTTGACAACTTCCCGGTTGAAGTT 62419
RESULT 11
AC098832 139028 bp DNA linear HTG 03-NOV-2001
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) chromosome 5 clone
QJ1268B08, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces.
ACCESSION
AC098832
VERSION
AC098832.1 GI:16603960
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HTG: HTGS, PHASE2.
Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 119028)
Chow, T.-Y., Hsing, Y.-I.-C., Liu, S.-M., Chen, C.-S., Shaw, J.-F.,
Chen, H.-H., Chao, Y.-T. and Wu, H.-P.
Oryza sativa BAC OJ1268B08 genomic sequence
Unpublished
2 (bases 1 to 119028)
Chow, T.-Y. and Hsing, Y.-I.-C.
Direct Submission
Submitted (03-NOV-2001) Institute of Botany, Academia Sinica, 128,
Section 2, Academia Road, Nankang, Taipei 11529, Taiwan
The nucleotide sequence of this BAC clone was generated by
combining Monsanto and ASPC-Taiwan sequencing data.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 47212: contig of 47212 bp in length
* 47213 47222: gap of unknown length
* 47223 50050: contig of 2828 bp in length
* 50051 50060: gap of unknown length
* 50061 63358: contig of 13298 bp in length
* 63359 63368: gap of unknown length
* 63369 111339: contig of 47971 bp in length
* 111340 111349: gap of unknown length
* 111350 119028: contig of 7679 bp in length.

FEATURES
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="5"
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Location/Qualifiers
BASE COUNT 32106 a 27418 c 26704 g 32758 t 42 others
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Alignment Scores:
Pred. No.: 5,77e-144 Length: 119028
Score: 1674.50 Matches: 317
Percent Similarity: 77.42% Conservative: 67
Best Local Similarity: 63.91% Mismatches: 105
Query Match: 62.48% Indels: 7
DB: 2 Gaps: 3
US-09-883-797-2 (1-520) x AC098832 (1-119028)
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Db 77746 CCGTGGCGGACTTCACCAATCGTGAAGCTCAAGTACGTGAAGCTGGGTACAC --- 77802
Qy 45 SerCysAsnValThrIleLeuPhePheLeuIleLeuProLeuThrGlyThrVal 64
Db 77803 -----TACCTCATCACACCGCGCTGCTGCTCGCCCGCTCCCGGCTCGTG 77856
Qy 65 LeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrpSerAsnGlnAla 84
Db 77857 GCGGGGACCTCTCCACCTTCACGCTGGCGGACCTCGCGGCTGGGCAAAAC ----- 77910
Qy 85 ValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeuThr 104
Db 77911 CTCAGTACAACTCGTCTCGCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCT 77970
Qy 105 LeuTyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysPro 124

Db	79051	GC	CAAGGGCGGATCAAGAGGGGACAGACGATGGCAGATCGCTTCGGCTCCGGGCTTC	79110
QY	485	LysCysAsnSerAlaValTrpLysAlaLeuArgProVal	-----SerThrGluGluMet	502
Db	79111	AAGTCAACAGCGCGTGTGGAGGGCGCTCCGGTCCGTCGACCGCGCAAGGAGAACAC	79170	
QY	503	ThrGlyAsnAlaTrpAlaGlySerLeuAspGlnTyrProValLysVal	518	
Db	79171	TTCACCAACCCGTTGATCGACGAGATCCACCGCTCCCGTCCGCCGTC	79218	
RESULT	12			
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LOCUS	ZMA292770	Zea mays mRNA	2018 bp	linear
DEFINITION	Zea mays mRNA for putative fatty acid longase (fae2 gene).			
ACCESSION	AJ292770			
VERSION	AJ292770.1	GI:9714500		
KEYWORDS	fae2 gene; fatty acid elongase.			
SOURCE	Zea mays.			
ORGANISM	Zea mays			
REFERENCE				
AUTHORS	1 (bases 1 to 2018) Schreiber, L., Skrabs, M., Hartmann, K., Becker, D., Cassagne, C. and Lessire, R.			
TITLE	Biochemical and molecular characterization of corn (Zea mays L.) root elongases			
JOURNAL	Biochem. Soc. Trans. 28 (5), 647-649 (2000)			
MEDLINE	21116804			
PUBMED	11171156			
REFERENCE	2 (bases 1 to 2018) Schreiber, L.			
AUTHORS	Direct Submission			
TITLE	Submitted (01-AUG-2000) Schreiber L., Botany II,			
JOURNAL	Julius-von-Sachs-Institute, Julius-von-Sachs-platz 3, D97082 Wuerzburg, GERMANY			
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ORIGIN				
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Score:	1658.00	Matches:	312	
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Best Local Similarity:	62.78%	Mismatches:	89	
Query Match:	61.87%	Indels:	9	

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QY	42	uHisAsnSerCysAsnValThrThrIleLeuPhePheLeuIleLeuProLeuThrGl 62			
Db	258	CCAC-----TACCTATATCCACGGGATCTACCTCTCTCTCTCGCGCTGATGGC 308			
QY	62	yThrValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuLeuTrpSerAs 82			
Db	309	GTCGTCGCGCTCGAGCTCTCCACCGCTCCCGCGATCATGCTCGCGACCTCGCG 363			
QY	82	nGlnAlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheVa 102			
Db	364	-GAGCAGCTCCGGTTCACCTCTCTCCGCTCGCTCGCTCCACGCTGCTCTCTCT 422			
QY	102	lLeuThrLeuTyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTy 122			
Db	423	CTCCACCGTTTACTCTCTCCACCGCGCGCGCTGACTGCTCGACTTCGCTGCTA 482			
QY	122	rLysProGluAspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAs 142			
Db	483	CAAGCCGGAGTCGCGGCAAGTCACGCGCGAGACCTTCATGCACTGCTCCAAAGCTCAC 542			
QY	142	nGlySerPheThrAspThrValGlnPheGlnGlnArgIleSerAsnArgAlaGlyLe 162			
Db	543	CGGATCTCTACGGACGAGAACCTTCGAGTTCCACGCGAAGATCTCGAGCGCTCCGGCT 602			
QY	162	uGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProProLysLeuAsnMetSe 182			
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QY	182	rGluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLy 202			
Db	663	CGAGCGCGTAAAGAGCGCGCGCGCTCATGTTCCGCGCCATCGACCAAGCTCTCGAGAA 722			
QY	202	sThrGlyIleLysProAlaGluValGlyIleLeuLeuValAsnCysSerLeuPheAsnPr 222			
Db	723	GACCGGTGTACGCCCAAGGACATGTTGTCTTAGTGTCACTGACGACCTGTTCAACCC 782			
QY	222	oThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSe 242			
Db	783	GAGCGCGTCTGCTCAGCATGTTGCTGAACCATTTACAAGCTGAGGGGGAATATTGTGAG 842			
QY	242	rTyrAsnLeuGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAs 262			
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QY	262	nLeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLe 282			
Db	897	TCTGCTGCAAGTGCACCCCACTCTACGCCCTGTTGATCAGCATGGAGAACATCACACT 956			
QY	282	uAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGl 302			
Db	957	GAATGGTACTTTGGGAACAACCGGTCCTGTTGTCGAATTTGCTCTTCGGATGGG 1016			
QY	302	yGlyAlaAlaIleLeuLeuSerAsnArgArgGlnAspArgLysLysSerLysTyrSerLe 322			
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QY	322	uValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysValTyrGl 342			
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QY	342	nLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAl 362			
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QY	402	oTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAl 422			
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QY	422	aValLeuAspGluValGlnLysAsnLeuAspLysAspTyrPheHisMetGluProSerAr 442			
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QY	442	gMetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTyrPheHisMetAlaTy 462			
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QY	462	rThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTyrGlnIleAlaPheGlySe 482			
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QY	482	rGlyPheLysCysAsnSerAlaValTyrLysAlaLeuArgProValSerThrGluGluMe 502			
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QY	502	tThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal 518			
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LOCUS		Arabidopsis thaliana chromosome 2 clone F18A8 map B68, complete			
DEFINITION		sequence.			
ACCESSION	AC003105				
VERSION	AC003105.3	GI:20197019			
KEYWORDS	HTG.				
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ORGANISM	Arabidopsis thaliana				
REFERENCE					
AUTHORS					
JOURNAL					


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Alignment Scores:		
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Best Local Similarity:	61.41%	101
Query Match:	61.16%	6
DB:	8	3
	Length:	
	Matches:	
	Conservative:	
	Mismatches:	
	Indels:	
	Gaps:	

ПС-09-883-797-2 (1-520) x AC003105 (1-95167)

QY	24	ArgArgLeuProAspLeuThrSerVallysLeuLysTyrVallysLeuGlyLeuHis	43
DB	128	CGTAATCTACCTGATTTCAAAAAATCAGTGAAGCTTAATATGTGAAGCTTGGTTACCAT	187
QY	44	AsnSerCysAsnValThrThrIleLeuPhePheLeuIleLeuProLeuThrGlyThr	63
DB	188	-----TACCTTATCACTCATGGAATGACCTTTCTCTCCCATTAGTACTTGTA	238
QY	64	ValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuThrPheSerAsnGln	83
DB	239	ATCGCTGCACAGATTCAACTTCTGTGTCAACGATCTCTGTAGCCCTCTGGGAGCAT---	295
QY	84	AlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeu	103
DB	296	---CTTCAGTACAACTTATCTCAGTGGTGTGTGTCTATGGCTGCTGTGTTCTTAAATG	352
QY	104	ThrLeuTyrValAlaAsnArgSerTyrProValTyrLeuValAspPheSerCysTyrLys	123
DB	353	ACTAATTACTTCATGACTCGACCCACTCTGTCTACTTGGTGAAGCTCTCGTGTCTTAAA	412
QY	124	ProGluAspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGly	143
DB	413	CCCGATGAGTCACGAAATGCATAAAAGATCTTTATGGATCGTCTTAACTCACTGGC	472
QY	144	SerPheThrAspAspThrValGlnPheGlnGlnArgIleSerAsnArgAlaGlyLeuGly	163
DB	473	TCTTTACACAGAGAGAATCTTGAGTTCACGCGTAAGATTCTACAACTGTGGGGCTCGG	532
QY	164	AspGluThrTyrLeuProArgGlyIleThrSerThrProProlsLeuAsnMetSerGlu	183
DB	533	GAATCGACTACTTACCCGAGGTGTACTTAATGTTCCGCTAACCCGTGTATGAAGAA	592
QY	184	AlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLysThr	203
DB	593	GCTCGAAAGAGCGCGAGACTGTATGTTGGAGCTATTGATGAGCTTCTTCCGAAGACG	652
QY	204	GlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnProThr	223
DB	653	AATGTGAACCCGAGGATATGGGATCTTGATTTAACTGTAGTTTGTAAACCCGACA	712
QY	224	ProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSerTyr	243
DB	713	CCTTCGTATCTGCTATGGTGTTAATCACTATAAGCTCCGCGGAATATACTTAGTTAC	772
QY	244	AsnLeuGlyGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnLeu	263
DB	773	AACTTGGGAGGAATGGGTTCAGTGCCTGGTTGATTTCTATTGATCTTGGCAACATCT	832

QY	264	LeuLysAlaAsnProAsnSerTyrAlaValValValSerThrGluAsnIleThrLeuAsn	283
DB	833	CTTCACTCTATTCCCAACACTTATGCAATGGTGAATAGTAGTGGAGAACAATTACCTTGAAC	892
QY	284	TtpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGlyGly	303
DB	893	TGGTATTTCGGGATGACCGTCAAGCTTGTCTTAATTTGCTGTTTGAATGGGAGGT	952
QY	304	AlaAlaIleLeuLeuSerAsnArgGlnAspArgLysLysSerLysTyrSerLeuVal	323
DB	953	GCAGCGATTCTCTTTTCGACAAAGATGGACAGAAGAAGATCGAATAATTCAGCTTGTT	1012
QY	324	AsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysValTyrGlnLys	343
DB	1013	GATACGCTTAGGACTCACAAAGGAGCTGATGAAGTCTTTTGGTTGGCATAAATCAAGAA	1072
QY	344	GluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAlaGly	363
DB	1073	GAGGATTCGCCAAGTAAAGATTGGTGTACCTTGTGGAAGAAGCTTATGCGTGTTCGGGT	1132
QY	364	AspAlaLeuLysThrAsnIleThrLeuGlyProMetValLeuProLeuSerGluGln	383
DB	1133	GATGCTCTCAAGACAAATATTACGACGTTAGCACCTGTTTACCGACATCTGAACAG	1192
QY	384	LeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysValLysProTyr	403
DB	1193	CTTCTGTCTTTCGCAACGTTAGTGGGAAGAAACTCTTCAAGATGAAGATCAAGCCTTAC	1252
QY	404	IleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAlaVal	423
DB	1253	ATCCAGACTTCAAACTAGCGTTTGGAGCATTTCTGCATCCACGAGGAGGAGCGTGT	1312
QY	424	LeuAspGluValGlnLysAsnLeuAspLeuLysAspTyrHisMetGluProSerArgMet	443
DB	1313	CTTGATGAATTGGAGAACTTGAAACTTCACAGATGGCATATGAGGCCCTCGAGGATG	1372
QY	444	ThrLeuHisArgPheGlyAsnThrSerSerSerLeuTyrTrpGluMetAlaTyrThr	463
DB	1373	ACACTCTACCGCTTTGGTAAACGCTCCAGTCTCTTCTTGTGTATGAATTAGCATATAGT	1432
QY	464	GluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySerGly	483
DB	1433	GAGGCCAAAGAGAGATCAAGAAAGTGATGAATTTGGCAGATAGCTTTTGGTTCGGGG	1492
QY	484	PheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMetThr	503
DB	1493	TTCAAGTCAACAGCTCGGTTTTGGAGCGGTAAAGTCGGTCAACCCCTCAAGAAA---GAG	1549
QY	504	GlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal	518
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DEFINITION			
ACCESSION			
AF424620.1			
VERSION			
FLI CDNA.			
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SOURCE			
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ORGANISM			
Arabidopsis thaliana			
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.			
REFERENCE			
1 (bases 1 to 1803)			
Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C.,			
Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D.,			
Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A.,			
Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X.,			
Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J.,			
Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A.,			
Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S.,			
Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.			


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Db 393 CATTTCTCTCCGCCACTCGCCACCGCACTC-----TTAATCTCTCTCCACCGCT 446
QY 106 TyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysProGlu 125
Db 447 TACTTCACCCCGTCCCGCGGTCTCTCTCCGACTTCTCGTTACAAACGAGAC 506
QY 126 AspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPhe 145
Db 507 CTTTCACTGATCTGCACCTCGTGAACATTCATGGACAGATCTCAACGCTAGGCATCTC 566
QY 146 ThrAspaspThrValGlnPheGlnArgIleSerAsnArgAlaGlyLeuGlyAspGlu 165
Db 567 ACAGAAGACAACCTTAGCTTTTCCACAAAGATCTCGAAAGATCCGGTCTAGGTGAGAAA 626
QY 166 ThrTyrLeuProArgGlyIleThrSerThrProLysLeuAsnMetSerGluAlaArg 185
Db 627 ACTTACTTCCCTGAAGCTCTTCTCGTGTCTCTCTAATCTTGTATGGAAGACGGAGA 686
QY 186 AlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLysThrGlyIle 205
Db 687 AAGAGGCAGAAACAGTATCTCGGAGCTATTGACGGGTCTTTGAGAAGACCGGTGTG 746
QY 206 LysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnProThrProSer 225
Db 747 AAACCTAAGATATGGAATCCTTGGTGAATGTAGCTGTGTTTAAATCCAACACCGTCA 806
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QY 401 LysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGly 420
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QY 461 AlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPhe 480
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Job time : 3735 secs

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 08:32:32 : Search time 315 Seconds
(without alignments)
3717.585 Million cell updates/sec

Title: US-09-883-797-2

Perfect score: 2680

Sequence: 1 MDRRLTAEMAFRDSSAVI.....EMTGNWAGSIDQPVKKVQ 520

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=N_Geneseq_101002 -ORFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
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-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2680	100.0	1560	20	AA2323217	A. thaliana EL1 DN
2	1647	61.5	1747	21	AAC37360	Arabidopsis thalia
3	1639	61.2	1720	21	AAC47402	Arabidopsis thalia
4	1626	60.7	1821	21	AAC50606	Arabidopsis thalia
5	1619	60.4	1824	21	AAC39957	Arabidopsis thalia
6	1601	59.7	1732	16	AAQ90219	Condensing enzyme
7	1598	59.6	1807	20	AAZ28316	Fatty acyl-CoA elo
8	1595.5	59.5	2143	22	AAH50968	Ketoacyl ACP synth
9	1588.5	59.3	1587	21	AAC42814	Arabidopsis thalia
10	1563	58.3	1548	20	AA232223	Arabidopsis thalia
11	1531.5	57.1	1611	20	AA232221	A. thaliana EL7 DN
12	1531.5	57.1	1853	21	AAC50224	A. thaliana EL5 DN
13	1519.5	56.7	1783	16	AAT04124	Arabidopsis thalia
14	1519.5	56.7	1783	16	AAQ90208	Jojoba wax-synthas
15	1513.5	56.5	1819	21	AAC39559	Jojoba fatty acyl-
16	1510.5	56.4	1855	21	AAC37776	Arabidopsis thalia
17	1497	55.9	1733	14	AAQ42839	Arabidopsis thalia
18	1497	55.9	1733	16	AAT04123	Jojoba fatty acyl
19	1497	55.9	1733	16	AAQ90207	Jojoba wax-synthas
20	1442.5	53.8	1704	16	AAQ90217	Jojoba fatty acyl-
21	1441	53.8	1650	20	AA232220	Condensing enzyme
22	1438.5	53.7	1502	20	AA232222	A. thaliana EL4 DN
23	1438.5	53.7	1840	21	AAC4659	A. thaliana EL6 DN
24	1438.5	53.7	1857	21	AAC45219	Arabidopsis thalia
25	1438.5	53.7	3722	20	AAV84180	Arabidopsis thalia
26	1438	53.7	1949	21	AAC33574	Arabidopsis thalia
27	1438	53.7	2008	21	AAC49056	Arabidopsis thalia
28	1432	53.4	1810	16	AAQ90210	Brassica condensin
29	1426.5	53.2	1523	21	AAC39308	Arabidopsis thalia
30	1419.5	53.0	1464	21	AAC42778	Arabidopsis thalia
31	1419.5	53.0	2509	22	AA262693	Arabidopsis thalia
32	1401	52.3	1482	21	AA251486	Maize ZmKCS1 prote
33	1401	52.3	1954	21	AA250706	Maize ZmKCS1 prote
34	1392	51.9	1584	21	AA235525	Fatty acid elongas
35	1323.5	49.4	1512	20	AA23219	A. thaliana EL3 DN
36	1317.5	49.2	1521	24	AAD28518	A. thaliana FAEL-B
37	1314.5	49.0	1521	24	AAD28511	B. napus elongase
38	1313.5	49.0	1521	24	AAD28520	A. thaliana FAEL-B
39	1310.5	48.9	1521	24	AAD28507	A. thaliana FAEL-B
40	1308.5	48.8	1521	24	AAD28519	A. thaliana FAEL-B
41	1307.5	48.8	1521	24	AAD28510	A. thaliana FAEL-B
42	1307.5	48.8	1521	24	AAD28515	Brassica napus elo
43	1306.5	48.8	1524	24	AAD28516	Brassica napus fat
44	1306.5	48.8	1785	22	AAF61744	B. napus KCS cDNA
45	1306.5	48.8	1785	22	AAF61746	B. napus KCS cDNA

ALIGNMENTS

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XX AA2323217;
AC
XX 11-JUN-1999 (first entry)
DT
XX A. thaliana EL1 DNA.
DE
XX EL1; very long chain fatty acid; VLCFA; beta-keto acyl synthase;
KW plant; vegetable oil; lubricant; fuel; feedstock; plastic; cosmetic;
KW pharmaceutical; edible oil; ss.
XX
XX Arabidopsis thaliana.
XX
XX WO9854954-A1.
XX

Thu Feb 20 11:03:34 2003

us-09-883-797-2.p2n.rng

PD 10-DEC-1998.
 XX PF 01-JUN-1998; 98WO-US11384.
 XX PR 03-JUN-1997; 97US-0868373.
 XX (CRGI) CARGILL INC.
 PA (JAWO) JAWORSKI J G.
 PA (POST) POST-BEITTENMILLER MA.
 PA (TODD) TODD J.
 XX XX
 PI Jaworski JG, Post-Beittenmiller MA, Todd J;
 XX WPI: 1999-070227/06.
 DR P-PSDB: AAW93427.
 XX
 CC New isolated beta-keto acyl synthase polynucleotides - used
 CC particularly for the production of transgenic plants having altered
 CC levels of very long chain fatty acids in tissues
 CC
 CC Claim 9; Fig 3; 76pp; English.
 CC
 CC This invention describes the isolation of beta-keto acyl synthase
 CC proteins from Arabidopsis thaliana. The products of the invention
 CC can be used for producing vegetable oils having elevated levels of
 CC very long chain fatty acids (VLCFA) for use as e.g. lubricants, fuels
 CC and as a feedstock for plastics, pharmaceuticals and cosmetics. The
 CC products can also be used for producing oils having reduced levels of
 CC VLCFAs for use as edible oils. This sequence encodes ELL.
 CC
 XX Sequence 1560 BP; 420 A; 355 C; 378 G; 407 T; 0 other;
 SQ
 Alignment Scores:
 Pred. No.: 3,19e-273 Length: 1560
 Score: 2680.00 Matches: 520
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0
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 Db 61 AGAATTCGAAGAGCGTTTTCGGGATTTATTAACGTCCTTAAGCTCAAAATACGTGAAGCTT 120
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 Db 241 TCTAACACGGCGGTTCAACTCGACACGGCGGACGACACTTACCTGGTTTCTCTCTCC 300
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 QY 321 SerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysVal 340
 Db 961 TCGCTGGTCAAGCTGCTTGAACACATAAAGGATCAGACGACAAAGAACTACAATTCG 1020
 QY 341 TyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSer 360
 Db 1021 TACCAGAGGAAGACGAGAGGAAACAATCCGGTGCTCTCTTACGTAGAGAGCTCATGCT 1080
 QY 361 ValAlaGlyAspAlaLeuLysThrAsnIleThrLeuGlyProMetValLeuProLeu 380
 Db 1081 GTCGCGGAGACGCTCTGAAACAAACATCACGACTTTAGACCGATGGTTCTTCCATG 1140
 QY 381 SerGluGlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysVal 400
 Db 1141 TCAGAGCAGTTGATGTTCTTGAATTCCTTGGTCAAAAGGAAGATGTTCAAGTAAAGTT 1200
 QY 401 LysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGly 420
 Db 1201 AAACCGTATATCCGGATTCAGCTAGCTTTCGAGCATTTCTGTATTCACGAGAGGT 1260
 QY 421 ArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTTPHisMetGluPro 440
 Db 1261 AGACGCGTTCTAGCAAGAGTGCAGAAATCTTGTATCTCAAGGATTCGACATGGAACCT 1320
 QY 441 SerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTyrTyrGluMet 460
 Db 1321 TCTAGATGACTTTGACACATTTGGTAAACATTCGAGTACGCTGCTTGTATGAGATG 1380
 QY 461 AlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPhe 480
 Db 1381 GCTTATACCGAAGCTAAGGTCGGGTTAAAGCTGGTGACGACTTGGCAGATTCGGTTT 1440
 QY 481 GlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGlu 500
 Db 1441 GGATCGGGTTCAAGTGTATAGTTCGGGTTTGGAAAGCGTTTACGACCGGTTTCGACGGAG 1500
 QY 501 GluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysValValGln 520
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RESULT 2
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ID AAC37360 standard; DNA; 1747 BP.
XX
AC AAC37360;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 17094.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
PN EPI033405-A2.
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
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PR 16-AUG-1999; 99US-0148684.
PR 17-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.

PR	20-AUG-1999;	99US-0149929.	142	-----TACCTATCACACATGGAATGTACTCTCTCTCCCACTAGTACTGTGA	192
PR	23-AUG-1999;	99US-0149902.	64	ValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuPheSerAsnGln	83
PR	23-AUG-1999;	99US-0149930.	193	ATCGCTGCACAGATTCAACTTCTCCATCACCGATCTTCGAGAGCTCTGGGAGCAT---	249
PR	26-AUG-1999;	99US-0150566.	84	AlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeu	103
PR	27-AUG-1999;	99US-0151065.	250	---CTTCAGTACAATCTTATCTCAGTGGTGTGTCTCTCTCTCTCTCTCTCTCTCT	306
PR	27-AUG-1999;	99US-0151080.	104	ThrLeuTyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLys	123
PR	31-AUG-1999;	99US-0151438.	307	ACTATTACTTCTATGCTGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	366
PR	01-SEP-1999;	99US-0151930.	124	ProGluAspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGly	143
PR	10-SEP-1999;	99US-0153070.	367	CCCGATGAGTCACGAAATGCTTAAAGATCTTTATGATCGTCTTAAACTCACTGGG	426
PR	15-SEP-1999;	99US-0154018.	144	SerPheThrAspAspThrValGlnPheGlnArgIleSerAsnArgAlaGlyLeuGly	163
PR	16-SEP-1999;	99US-0154039.	427	TCTTTCACAGAGAGAACTCTTGAGTCCAGCGTAAGATTTCTACAACTTCGGGGCTGGG	486
PR	20-SEP-1999;	99US-0155139.	164	AspGluThrTyrLeuProArgGlyIleThrSerThrProLysLeuAsnMetSerGlu	183
PR	23-SEP-1999;	99US-0155486.	487	GAATCGACTTACTTACCCGAGGCTGACTCAATGTTCCGCTACCTGCTGTATGAAGAA	546
PR	24-SEP-1999;	99US-0156458.	184	AlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLysThr	203
PR	28-SEP-1999;	99US-0156569.	547	GCTCGAAAGAGAGCCGAGAGCTGTATGTTGGCGCTATGATGAGTCTTTCGGAAGAGC	606
PR	29-SEP-1999;	99US-0157117.	204	GlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnProThr	223
PR	04-OCT-1999;	99US-0157753.	607	AATGTGAACCCGAGGATATCGGATCTTGAATGTTAACTGTTAACTGTTAACTGTTAACT	666
PR	06-OCT-1999;	99US-0158029.	224	ProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSerTyr	243
PR	07-OCT-1999;	99US-0158232.	667	CTTCTGTTATCTGCTATGTTGTTTAACTATGATGATGATGATGATGATGATGATGATG	726
PR	12-OCT-1999;	99US-0158369.	244	AsnLeuGlyGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnLeu	263
PR	13-OCT-1999;	99US-0159293.	727	AACTTGGGAGGAAATGGGTTGCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	786
PR	13-OCT-1999;	99US-0159294.	264	LeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsn	283
PR	14-OCT-1999;	99US-0159330.	787	CTTCACCTCCATCCCAACACTTATGCAATGGTGATGATGATGATGATGATGATGATGATG	846
PR	14-OCT-1999;	99US-0159637.	284	TrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGlyGly	303
PR	14-OCT-1999;	99US-0159638.	847	TGGTATTTTCGGGAAATGACCGGTGCGAGCTTGTCTTAAATTTGTCTTAAATTTGTCTT	906
PR	18-OCT-1999;	99US-0160741.	304	AlaAlaIleLeuLeuSerAsnArgArgGlnAspArgLysLysSerLysTyrSerLeuVal	323
PR	21-OCT-1999;	99US-0160767.	907	GCAGCGATCTTCTTTCGAAACAAAGATGGGACAGAGAGATGCAAAATATGAGCTTGT	966
PR	21-OCT-1999;	99US-0160814.	324	AsnValValArgThrHisLysGlySerAspLysAsnTyrAsnCysValTyrGlnLys	343
PR	22-OCT-1999;	99US-0160980.	967	GATACGGTTAGGACTCACAAGGAGCTGATGATGATGATGATGATGATGATGATGATGATG	1026
PR	22-OCT-1999;	99US-0160981.	344	GluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAlaGly	363
PR	25-OCT-1999;	99US-0161404.	1027	GAGGATTCGGCAAGTAAGATCGGTGTACCCCTGTCGAAAGAACTTATGGCTGTGGCGGT	1086
PR	25-OCT-1999;	99US-0161405.	364	AspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeuProLeuSerGluGln	383
PR	26-OCT-1999;	99US-0161406.	1087	GATGCTCTAAAGACAAATATATAGGCTTAGGACCACTGGTCTTACCGACATCTGAACAG	1146
PR	26-OCT-1999;	99US-0161360.	384	LeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysValLysProTyr	403
PR	26-OCT-1999;	99US-0161361.	1147	CTTCTGTTCTTTCGCAACGTTAGTGGGAAGAAACTCTTCAAGATGAAGATCAAGCCATAT	1206
PR	28-OCT-1999;	99US-0161920.	404	IleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAlaVal	423
PR	28-OCT-1999;	99US-0161992.	1207	ATCCACGACTTCAAACTAGGTTTGACATTTCTGTCATCCACGCGGAGGAGAGCTGTT	1266

Alignment Scores:
 Pred. No.: 6,92e-164
 Score: 1647.00
 Percent Similarity: 78.59%
 Best Local Similarity: 61.62%
 Query Match: 61.46%
 DB: 21

US-09-883-797-2 (1-520) x AAC37360 (1-1747)
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 DB 82 CGTAATCTACTGATTTCAAAATATGAGTAAAGTATGTAAGCTTGGTATACCAT 141
 QY 44 AsnSerCysAsnValThrIleLeuPhePheLeuIleLeuProLeuThrGlyThr 63

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PR	03-AUG-1999;	99US-0147038.
PR	04-AUG-1999;	99US-0147204.
PR	05-AUG-1999;	99US-0147302.
PR	05-AUG-1999;	99US-0147192.
PR	05-AUG-1999;	99US-0147260.
PR	06-AUG-1999;	99US-0147303.
PR	06-AUG-1999;	99US-0147416.
PR	08-AUG-1999;	99US-0147493.
PR	09-AUG-1999;	99US-0147935.
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PR	10-AUG-1999;	99US-0148171.
PR	11-AUG-1999;	99US-0148319.
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PR	13-AUG-1999;	99US-0148565.
PR	13-AUG-1999;	99US-0148684.
PR	16-AUG-1999;	99US-0149368.
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PR	18-AUG-1999;	99US-0149426.
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PR	23-AUG-1999;	99US-0149902.
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PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
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PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	02-AUG-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161993.
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Alignment Scores:		
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Score:	1639.00	Matches: 304
Percent Similarity:	78.38%	Conservative: 84
Best Local Similarity:	61.41%	Mismatches: 101
Query Match:	61.16%	Indels: 6
DB:	21	Gaps: 3
US-09-883-797-2 (1-520) x AAC47402 (1-1720)		
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QY	44 AsnSerCysAsnValThrThrIleLeuPhePheLeuIleIleLeuProLeuThrGlyThr	63
Db	119 -----TACCATTATCACTCATCGAATGTACTTTCTCTCCCATATTACTTGTGA	169
QY	64 ValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuThrSerAsnGln	83
Db	170 ATCGCTGCACAGATTTCAACTTTCTCTGTACCGAGTCTTCGTAGCCTCTGGGAGCAT---	226
QY	84 AlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeu	103
Db	227 ---CTTCAGTACAATCTTATCTCAGTGGTGTGTTGTTCTATGCTGCTGTTCTTAAATG	283
QY	104 ThrLeuTyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLys	123
Db	284 ACTATTACTTTCATGACTCGACCACGCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	343
QY	124 ProGluAspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGly	143
Db</		

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Db 884 GCAGCGATTCTTCTTCGACAAACATGGGACAGAGAGATCGAAATATGAGCTTGT 943
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QY 344 GluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAlaGly 363
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QY 364 AspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeuProLeuSerGluGln 383
Db 1064 GATGCTCTAAAGACAAATATTACGACGTTAGGACCACTGGTTTACCGACATCTGAACAG 1123
QY 384 LeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLysValLysProTyr 403
Db 1124 CTTCGTCTTGTGCAACGTTAGTGGGAAGAAACTCTTCAAGATGAAGATCAAGCCTTAC 1183
QY 404 IleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAlaVal 423
Db 1184 ATCCAGACTTCAAACTAGCCTTTGAGCATTTCTGCATCCAGCGAGGAGGAGCTGTT 1243
QY 424 LeuAspGluValGlnLysAsnLeuLysLeuLysAspTrpHisMetGluProSerArgMet 443
Db 1244 CTTCATGAATGTCAGAGAACTTGAACACTCACAGATGGCATATGAGCCCTCGAGGATG 1303
QY 444 ThrLeuHisArgPheGlyAsnThrSerSerSerLeuTyrTrpTyrGluMetAlaTyrThr 463
Db 1304 ACATCTACCGTTTGTGTAAACACGTCACGTTCTTCTTGTGTGATGAATAGCATATAGT 1363
QY 464 GluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySerGly 483
Db 1364 GAGCCAAAGAGGAGGATCAAGAAAGGTAGATAATTTGGCAGATAGCTTTTGTTCGGGG 1423
QY 484 PheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluLysMetThr 503
Db 1424 TTCAAGTGCACACGCTGGTTGGAGAGCGGTAAAGCTGGTAAACCCCTAAGAAA---GAG 1480
QY 504 GlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal 518
Db 1481 AGAACCCATGGATGGATGAATATCATGAGTTCCAGTTGAAGTC 1525

RESULT 4
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ID AAC50606 standard; DNA; 1821 bp.
XX
AC AAC50606;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 65464.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
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QY 326 ValArgThrHisLysGlySerAspLysAsnTyrAsnCysValTyrGlnLysGluAsp 345
Db 1100 GTCCGTACCCAAAGAGAGCTCATGACCAACGATTTGGCTGTGTTCACCAAGAGAGAC 1159
QY 346 -----GluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerVal 361
Db 1160 AACACGCGAGAGAAACCGCAAAATCGAGTGTCCCTCTCTAAACCAATGAGGATA 1219
QY 362 AlaGlyAspAlaLeuLysThrAsnIleThrLeuGlyPrometValLeuProLeuSer 381
Db 1220 GCTGGAGAGCTCTCAAGACAAACATCAAACTCTCGACCACTAGTCTACCAATGCC 1279
QY 382 GluGlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeu---LysVal 400
Db 1280 GAACAACTTCTTTTCGCGACTCTGTGGCCCGAAAGTCTTCAAGTCAAGAAATA 1339
QY 401 LysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGly 420
Db 1340 AAGCTTACATTCCTGATTTCAAGTAGCTTCGAGCATTTCTGTATCCACGGGAGGT 1399
QY 421 ArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluPro 440
Db 1400 AGAGCCGTGCTCCAGAGATGTAGAGAACTTGGATTTATCCGATGCGACATGGAGCA 1459
QY 441 SerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTrpTyrGluMet 460
Db 1460 TCGAGGATGACGTTGAACCGTTTGGTAAACATTCGAGTAGCTCACCTTGGTATGAGCTT 1519
QY 461 AlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPhe 480
Db 1520 GCGTATAGTAGAAGCTAAAGGAGGATTAAGAGAGAGATAGGACTTGGCAGATTCGCTTT 1579
QY 481 GlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGlu 500
Db 1580 GGATCGGGTTTAAAGTGTATAGTGCAGTTTGGAAAGCTTGGAGACGATGTATCCCAATG 1639
QY 501 GluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal 518
Db 1640 GACGAGAGACTAATCCATGGATGTAGATTCATGATGATCTTCTGTTCAAGTT 1693
RESULT 5
AAC39957
ID AAC39957 standard; DNA; 1824 BP.
XX AC AAC39957;
XX AC AAC39957;
DT 17-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 26523.
XX

Hybridisation assay; genetic mapping; gene expression control;
protein identification; signal transduction pathway;
metabolic pathway; promoter; termination sequence; ss.
Arabidopsis thaliana.

PN EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 08-APR-1999; 99US-0128234.
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PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
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PR 04-MAY-1999; 99US-0132484.
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PR 06-MAY-1999; 99US-0132486.
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PR 14-MAY-1999; 99US-0134370.
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PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
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PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.

QY 106 TyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysProGlu 125
 Db 438 TACTTACCACCGCTCTCCGCGTGTCTTCTCTCAGCTTCGTGTCTTACAAACACGAC 497
 QY 126 AspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPhe 145
 Db 498 CTTTCACTGATCTGCACTCGTGAACATTCATGGACAGATCTCAACGCTGTAGGCATCTC 557
 QY 146 ThrAspThrValGlnPheGlnGlnArgIle-SerAsnArgAlaGlyLeuGlyAspG1 165
 Db 558 ACAGAGAGCACTTACCTTCCAAACAAAGATCTCGAAAGATCGGCTAGGTCTAGGTCAAG 617
 QY 165 uThrTyrLeuProArgGlyIleThrSerThrProLysLeuAsnMetSerGluAlaAr 185
 Db 618 AACTTACTTCCCTGAAGCTCTTCTCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 677
 QY 185 gAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLysThrGlyI1 205
 Db 678 AAAGAGGACAGAAACAGTATGTTGCGAGCTATTGACGGGTCTTTGAGAAGACCGGTGT 737
 QY 205 elysProAlaGluValGlyIleLeuLeuValAsnCysSerLeuPheAsnProThrProSe 225
 Db 738 CAACCTTAAGATATTGAATCTTGTGGTGAATGTTAGTCTTGTATTAATCAACACCGTC 797
 QY 225 rLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSerTyrAsnLe 245
 Db 798 ACTTCTGCTATGATTTGTAATAGTATAAGCTTAGAGCAACATTTTGTAGCTAATCT 857
 QY 245 uGlyGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAsnLeuLeu 265
 Db 858 TGGTGGATGGATGATGCTGGCTTATCTCCATTCATCTCGTAAACAGATGCTTCA 917
 QY 265 sAlaAsnProAsnSerTyrAlaValAlaValSerThrGluAsnIleThrLeuAsnTrpTy 285
 Db 918 GGTGCAACCAAACTCATACGACCTAGTGGTGCAGCACAGACATACCCCTAACTGGTA 977
 QY 285 rPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGlyGlyAlaAl 305
 Db 978 CTTAGGCAACGACGATCAATGCTTCTATCTAATTTGTATCTTCCGTATGCGGAGCGC 1037
 QY 305 aIleLeuLeuSerAsnArgArgGlnAspArgLysLysSerLysTyrSerLeuValAsnVa 325
 Db 1038 GGTACTTCTCGAACCGCTCTCTGATCGCAGCGCTTCAAAATATCAGCTCATCCATAC 1097
 QY 325 lValArgThrHisLysGlySerAspLysAsnTyrAsnCysValTyrGlnLysGluAs 345
 Db 1098 CGTCCGTACCAACAAAGAGCTGATGACAAACATCAACTCTCGGACCACTAGTCTTCA 1157
 QY 345 p-----GluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerVa 361
 Db 1158 CAACAACGCAAGAAACCGCAAGATCGGAGTCTCACTCTCTCTCTCTCTCTCTCTCTCT 1217
 QY 361 lAlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeuProLeuSe 381
 Db 1218 AGCCGGAGAGTCTCAAGCAAAACATCAACTCTCGGACCACTAGTCTTCACTTCACTTCA 1277
 QY 381 rGluGlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeu---LysVa 400
 Db 1278 CGAACAACTTCTCTTTCGCGACTCTTGGGCGCCGAAAGTCTTCAAGTCAAGAAAT 1337
 QY 400 llysProThrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyG1 420
 Db 1338 AAAGCTTACATCTCTGACTTCAAGTAGCTTTCGAGCATTTCTGTATCCACCTGGAGG 1397
 QY 420 YArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluPr 440
 Db 1398 TAGACCGGTGCTTGACGAGATGAGAAAGAACTTGGATTTATCGAATGCGACATGGAGCC 1457
 QY 440 oSerArgMetThrLeuHisArgPheCysIleAsnThrSerSerSerSerLysTrpTrpGluMe 460
 Db 1458 ATCGAGGATGAGTTGAACCGGTGGTGAACACTTTCGAGTAGCTCACTTGTGTATGAGCT 1517
 QY 460 tAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPh 480

Db 1518 TCGGTATAGTGAAGCTAAAGGAGGAGTAAAGAGAGGAGATAGGACTTGGCAGATTGCTTT 1577
 QY 480 eGlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrG1 500
 Db 1578 TGGATCGGGTTTAAAGTGTAAACAGTGCAGTCTTGGAAAGCTTTTGAGAAGGATTGATCCAAT 1637
 QY 500 uGluMetThrGlyAsnAlaTTPAlaGlySerIleAspGlnTyrProValLysVal 518
 Db 1638 GGACGAGAGACTAATCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1692

RESULT 6
 ID AAQ90219 standard; cDNA; 1732 BP.
 XX
 AC AAQ90219;
 XX
 DT 04-DEC-1995 (first entry)
 XX
 DE Condensing enzyme clone Lunaria 27.
 XX
 KW Lunaria; condensing enzyme; ss.
 XX
 OS Lunaria annua.
 XX
 FH Key Location/Qualifiers
 FT CDS 19..1614
 FT /*tag= a
 XX
 PN W09515387-A.
 XX
 PD 08-JUN-1995.
 XX
 PF 30-NOV-1994; 94WO-US13686.
 XX
 PR 23-JUN-1994; 94US-0265047.
 PR 30-NOV-1993; 93US-0160602.
 XX
 PA (CALJ) CALGENE INC.
 XX
 PI Lardizabal KD, Lassner MW, Metz JG;
 XX
 DR WPI: 1995-215267/28.
 DR P-PSDB; AAR77173.
 XX
 XX Production of very long chain fatty acid(s) in plant(s) - to produce
 PT drought and stress resistant transgenic plant(s)
 XX
 PS Claim 9; Figure 14; 149pp; English.
 XX
 CC The CE15 and CE20 Brassica cDNA sequences (see AAQ90210,Q90211
 CC and AAQ90212) and the condensing enzyme encoding sequence from
 CC Jojoba (AAQ90208) were used in determining primers AAQ90221-
 CC AAQ90225 from conserved AAs. These primers were variously used to
 CC PCR (RT-PCR) amplify fragments from RNA isolated from developing
 CC seeds of Lunaria annua, Tropaeolu majus (Nasturtium), and
 CC green liliques of Arabidopsis thaliana. The primers most
 CC successfully utilised were AAQ90221 and AAQ90222. These primers were
 CC used to produce three clones encoding a portion of the elongase
 CC condensing enzyme from Arabidopsis. From Lunaria a single clone
 CC was identified, LUN CE8. A cDNA library from RNA isolated from
 CC developing seeds of Lunaria was constructed, and LUN CE8 was used
 CC to screen this library. Three classes of cDNA clones were isolated,
 CC Lunaria 1, Lunaria 5 and Lunaria 27. Lunaria 5 shares approx.
 CC 85% homology with the Brassica CE20 clones, and it is suggested
 CC that it is active in seed oil fatty acid elongation.
 XX
 SQ Sequence 1732 BP; 505 A; 435 C; 317 G; 475 T; 0 other;

Alignment Scores:
 Pred. No.: 5.01e-159 Length: 1732
 Score: 1601.00 Matches: 308
 Percent Similarity: 76.69% Conservative: 77

XX

PI Cahoon EB, Hitz WD, Kinney AJ, Vollmer SJ;

XX WPI; 1999-591101/50.

DR P-PSDB; AAY39362.

XX Nucleic acid fragments useful in the production of industrial agents

PT for eg. lubricants or cosmetics -

XX PS Claim 7; Page 49; 54pp; English.

XX This is the nucleotide sequence of the entire Limnanthes fatty acyl-CoA
 CC elongase. This enzyme prefers palmitoyl-CoA (16:0-CoA) as its substrate
 CC instead of oleoyl-CoA (18:1-CoA) the usual substrate for the known plant
 CC fatty acid elongase. Fatty acids are used in plant membranes and in
 CC neutral lipids that are formed for the storage of energy in developing
 CC seed tissue. This nucleotide sequence can be linked to regulatory
 CC sequences and used to transform host cells. This invention also consists
 CC of the Limnanthes douglasii delta-5 acyl-CoA desaturase cDNA (AAZ28315).
 CC The delta-5 desaturase introduces a double bond at the delta 5 position
 CC of a C20 fatty acid. Delta-5 desaturase is an enzyme which is able to
 CC further desaturate mono-unsaturated fatty acids to make poly-unsaturated
 CC fatty acids. The nucleic acid sequences of the delta-5 desaturase and
 CC fatty acid biosynthetic pathways, allowing changes to be made in the
 CC fatty acid composition of plants and or oils and to introduce new
 CC pathways in to oil seeds in order to produce new biopolymers from
 CC acyl-CoA. The oils and fatty acids produced by the genetically engineered
 CC plants have potential for use as industrial agents including lubricants,
 CC greases, plastics, inks, cosmetics and surfactants. Polyestolides derived
 CC from the 20:1 delta-5 fatty acids of Limnanthes biodegrade slower than
 CC those derived from soybean oils or oleic oils, and thus will produce
 CC industrial products with a longer shelf life.

XX SQ Sequence 1807 BP: 496 A; 359 C; 412 G; 534 T; 6 other;

Alignment Scores:

Pred. No.: 111e-158 Length: 1807
 Score: 1598.00 Matches: 296
 Percent Similarity: 76.25% Conservative: 86
 Best Local Similarity: 59.08% Mismatches: 113
 Query Match: 59.63% Indels: 6
 DB: 20 Gaps: 3

US-09-883-797-2 (1-520) x AAZ28316 (1-1807)

QY 19 ValIleArgIleArgArgLeuProAspLeuLeuThrSerValLysLeuLysTyrVal 38
 Db 112 ATCGCAACCGTGAAACACACACTACCTGATTTAAACATATCAATAAATTAACACAGTG 171
 QY 39 LysLeuGlyLeuHisAsnSerCysAsnValThrThrIleLeuPheLeuIleLeu 58
 Db 172 AAATCGGTTACCAT-----TACCTGATCATCCCATGGAATGTACCTGTGTCCT 222
 QY 59 ProLeuThrGlyThrValValGlnLeuThrGlyLeuThrPheAspThrPheSerGlu 78
 Db 223 CTTCTCGGACTAGTCTCTCTCGTCAAACTCAACTTTGTCCTCAAGATTTCAACGAC 282
 QY 79 LeuTrpSerAsnGlnAlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPhe 98
 Db 283 ATCTCG-----GACAGCTTCAGTNNAAATCTCATNCTGCTGTTTTCATCAACACTT 336
 QY 99 LeuSerPheValLeuThrThrValAlaAsnArgSerLysProValLysLeuValAsp 118
 Db 337 CTGTGCTCTTACTTATCTTACITCATGACTCGTCCGAGCGCGTATTTTGTGATGGAT 396
 QY 119 PheSerCysTyrLysProGluAspGluArgLysIleSerValAspSerPheLeuThrMet 138
 Db 397 TTCGGTCTATAAACCCGACCAACTCGAAATCTACTAGAACATTTTATGAAGTGT 456
 QY 139 ThrGluGluAsnGlySerPheThrAspThrValGlnPheGlnGlnArgIleSerAsn 158
 Db 457 GGTGAGAGTTTGGGCTCTTTTACGGAGGATTAATTCGATTTTTCAGAGGAATTAGTCGCA 516

QY 159 ArgAlaGlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProLys 178
 Db 517 CGATCTGGACTTGGTGATCTACGTATTTACCTGAAGCTATCGGTATCCCGGTCAT 576
 QY 179 LeuAsnMetSerGluAlaArgAlaGluAlaValMetPheGlyAlaLeuAspSer 198
 Db 577 CCGTCAAGAACTGCGAGAGAGAGCTGAGTGTGTGATGTTGGTGGGATGATCAA 636
 QY 199 LeuPheGluLysThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSer 218
 Db 637 CTTTGGAGAGACAAAGGTGAATCCGAAGGATATAGGATCTTGGTGTGTTAATTCGAC 696
 QY 219 LeuPheAsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGlu 238
 Db 697 CTGTTTGTAGTCCGACTCCCTCGTCTCGTGAATGTTTAAACCACTATAAATCCGTTGG 756
 QY 239 AspIleLysSerTyrAsnLeuGlyMetGlyCysSerAlaGlyLeuLeuSerIleAsp 258
 Db 757 AACATTAACTACATCTAGGCGGAATGGTTGAGTGTGTTAATTTTCGGTGCAC 816
 QY 259 LeuAlaAsnAsnLeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGlu 278
 Db 817 TTAGCTAAAGACTTTCGAGACAAATCCAAACACTTACGCTTTAGTTATGACCACTGAA 876
 QY 279 AsnIleThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIle 298
 Db 877 AATATCACACTAACTGGTACATGGCAATGACCGGTCCAAACTCGTCCCAATTTGCTT 936
 QY 299 PheArgMetGlyGlyAlaAlaIleLeuLeuSerAsnArgGlnAspArgLysLysSer 318
 Db 937 TTCGGATGGAGAGCTGCGGTCTTGTATCAAAACAAACCTCTGATAAGAAAGATCG 996
 QY 319 LysTyrSerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsn 338
 Db 997 AAGTATCAGTTGTTACTACCGTCCGAGGACAAAGGTGCTGACGATAATTTGTCAGGT 1056
 QY 339 CysValTyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeu 358
 Db 1057 TGCATATCCCAAGAAGAACTCCAAACGCAAAATCGTGTAAACCTCTCCAAATCTA 1116
 QY 359 MetSerValAlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeu 378
 Db 1117 ATGGCGTCCGAGGAGCGCTTAAGACTTAACATCAACGCTGCTGCTGCTGCTGCTT 1176
 QY 379 ProLeuSerGluGlnLeuMetPheLeuIleSerLysValLysArgLysMetPheLysLeu 398
 Db 1177 CCAATGTCCGAACAACCTTTTGTGTTTTCGCCACGCTGTTGCTCGAAAGTTTTCAGAG 1236
 QY 399 LysValLysProTyrTrpIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAla 418
 Db 1237 AAAATTAGCCCTACATCCGACTTAAACCTAGCTTTTGTATCATTTCTGTTATCATGCG 1296
 QY 419 GlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTTPHisMet 438
 Db 1297 GGTGTCGAGCTGTTTGGACGAGCTTGAGAGAAATTTGACGTTTCAAGCTGGCATCTA 1356
 QY 439 GluProSerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerLeuTrpTyr 458
 Db 1357 GAGCGCTGAGAAATGACGTTTATCGGTTTGGTAAATACGTCGAGTAGTACTTTGTGTAC 1416
 QY 459 GluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIle 478
 Db 1417 GAGCTGGCTATTCGGAAGCAAGGAGGAGGATTAAGAAAGAAAGAGAGTTTGGCAGATA 1476
 QY 479 AlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSer 498
 Db 1477 GGGTTTGGTCTCGGTTTAAATGTAATAGTGTCTGCGAAAGCCTTAAAGAGCGTGTAT 1536
 QY 499 ThrGluGluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal 518
 Db 1537 CCAAGAAA---GAGACAACTCCATGGATGGATGATGATCCACCATTTCCGCTGCTGTT 1593

[illegible]

US-09-883-797-2 (1-520) x AAH50968 (1-2143)

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QY 367 LysThrAsnIleThrThrLeuGlyProMetValLeuProLeuSerGluGlnLeuMetPhe 386
Db 1334 AAAGCCAAACATCACCGCTAGGCCGCTCGTCTCTCTCCGAACAGCTGCTCTT 1393
QY 387 LeuIleSerLeuValLysArgLysMetPheLysLeuLysValLysProTyrIleProAsp 406
Db 1394 TTCAGCACGCTCGCTCGCTCGGAAGCTTCAACATGAAGCTCAAGCTTATATCTCGAT 1453
QY 407 PheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAlaValLeuAspGlu 426
Db 1454 TTCAGCTGGCTTCGACGCTCTCGATCCACGCGCGGAGGCGGCTGATCGACGAG 1513
QY 427 ValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArgMetThrLeuHis 446
Db 1514 CTTGAGAAAGCTGCACTACTCCGCGACACTGTGAGCGCTGACGAATGACCTCCAC 1573
QY 447 ArgPheGlyAsnThrSerSerSerLeuTyrTrpTyrGluMetAlaTyrThrGluAlaLys 466
Db 1574 AGATTGGTAATACGCTCTCTCTCTGATCTGTGAGCGCTGACGAATGACCTCCAC 1633
QY 467 GlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySerGlyPheLysCys 486
Db 1634 GGGCGCATCGCGGAGGCAACGAGTGTGGCAAAATGCTTTGGGAGCGGTTTAAGTGC 1693
QY 487 AsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMetThrGlyAsnAla 506
Db 1694 AATAGCGCTGTCTGCGAGCATTCGCAAAACATCAAGCGCTCGGAGAG-----TCGCCG 1747
QY 507 TrpAlaGlySerIleAspGlnTyrProValLysVal 518
Db 1748 TGGGCTCATTTATCGATGAGTACCTCAACATGTG 1783

RESULT 9
AAC42814
ID AAC42814 standard; DNA; 1587 BP.
XX AC AAC42814;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 36950.
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence, ss.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.
XX PR 09-MAR-1999; 99US-0123548.
XX PR 23-MAR-1999; 99US-0125788.
XX PR 25-MAR-1999; 99US-0126264.
XX PR 29-MAR-1999; 99US-0126785.
XX PR 01-APR-1999; 99US-0127462.
XX PR 06-APR-1999; 99US-0128234.
XX PR 08-APR-1999; 99US-0128714.
XX PR 16-APR-1999; 99US-0129845.
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XX PR 16-JUN-1999; 99US-0139453.
XX PR 17-JUN-1999; 99US-0139492.
XX PR 18-JUN-1999; 99US-0139454.
XX PR 18-JUN-1999; 99US-0139455.
XX PR 18-JUN-1999; 99US-0139456.
XX PR 18-JUN-1999; 99US-0139457.
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XX PR 18-JUN-1999; 99US-0139459.
XX PR 18-JUN-1999; 99US-0139460.
XX PR 18-JUN-1999; 99US-0139461.
XX PR 18-JUN-1999; 99US-0139462.
XX PR 18-JUN-1999; 99US-0139463.
XX PR 18-JUN-1999; 99US-0139750.
XX PR 21-JUN-1999; 99US-0139763.
XX PR 22-JUN-1999; 99US-0139817.
XX PR 23-JUN-1999; 99US-0139899.
XX PR 23-JUN-1999; 99US-0140353.
XX PR 24-JUN-1999; 99US-0140354.
XX PR 28-JUN-1999; 99US-0140695.
XX PR 29-JUN-1999; 99US-0140823.
XX PR 30-JUN-1999; 99US-0140991.
XX PR 01-JUL-1999; 99US-0141287.
XX PR 01-JUL-1999; 99US-0141842.
XX PR 02-JUL-1999; 99US-0142154.
XX PR 06-JUL-1999; 99US-0142055.
XX PR 08-JUL-1999; 99US-0142390.
XX PR 09-JUL-1999; 99US-0142803.
XX PR 12-JUL-1999; 99US-0142920.
XX PR 13-JUL-1999; 99US-0142977.
XX PR 14-JUL-1999; 99US-0143542.
XX PR 15-JUL-1999; 99US-0143624.
XX PR 16-JUL-1999; 99US-0144005.
XX PR 16-JUL-1999; 99US-0144085.
XX PR 19-JUL-1999; 99US-0144086.
XX PR 19-JUL-1999; 99US-0144325.
XX PR 19-JUL-1999; 99US-0144331.
XX PR 19-JUL-1999; 99US-0144332.
XX PR 19-JUL-1999; 99US-0144333.
XX PR 19-JUL-1999; 99US-0144334.
XX PR 19-JUL-1999; 99US-0144335.
XX PR 20-JUL-1999; 99US-0144352.
XX PR 20-JUL-1999; 99US-0144632.
XX PR 21-JUL-1999; 99US-0144884.
XX PR 21-JUL-1999; 99US-0144814.
XX PR 21-JUL-1999; 99US-0145086.
XX PR 22-JUL-1999; 99US-0145088.
XX PR 22-JUL-1999; 99US-0145085.
XX PR 22-JUL-1999; 99US-0145087.
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PR	22-JUL-1999;	99US-0145089.	PR	21-OCT-1999;	99US-0160814.	PR	21	9.22e-158	Length:	1587
PR	23-JUL-1999;	99US-0145192.	PR	22-OCT-1999;	99US-0160815.	PR	21	1588.50	Matches:	305
PR	23-JUL-1999;	99US-0145145.	PR	22-OCT-1999;	99US-0160980.	PR	21	75.25%	Conservative:	75
PR	23-JUL-1999;	99US-0145218.	PR	22-OCT-1999;	99US-0160981.	PR	21	60.40%	Mismatches:	106
PR	23-JUL-1999;	99US-0145224.	PR	22-OCT-1999;	99US-0160989.	PR	21	59.27%	Indels:	19
PR	26-JUL-1999;	99US-0145276.	PR	25-OCT-1999;	99US-0161404.	PR	21	21	Gaps:	6
PR	27-JUL-1999;	99US-0145291.	PR	25-OCT-1999;	99US-0161405.	PR	21			
PR	27-JUL-1999;	99US-0145293.	PR	25-OCT-1999;	99US-0161406.	PR	21			
PR	27-JUL-1999;	99US-0145294.	PR	26-OCT-1999;	99US-0161359.	PR	21			
PR	27-JUL-1999;	99US-0145295.	PR	26-OCT-1999;	99US-0161360.	PR	21			
PR	02-AUG-1999;	99US-0146386.	PR	26-OCT-1999;	99US-0161361.	PR	21			
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PR	02-AUG-1999;	99US-0146389.	PR	28-OCT-1999;	99US-0161922.	PR	21			
PR	03-AUG-1999;	99US-0147038.	PR	28-OCT-1999;	99US-0161993.	PR	21			
PR	04-AUG-1999;	99US-0147204.	PR	29-OCT-1999;	99US-0162142.	PR	21			
PR	04-AUG-1999;	99US-0147302.	PR			PR	21			
PR	05-AUG-1999;	99US-0147192.	PR			PR	21			
PR	05-AUG-1999;	99US-0147260.	PR			PR	21			
PR	06-AUG-1999;	99US-0147303.	PR			PR	21			
PR	06-AUG-1999;	99US-0147416.	PR			PR	21			
PR	09-AUG-1999;	99US-0147493.	PR			PR	21			
PR	09-AUG-1999;	99US-0147935.	PR			PR	21			
PR	10-AUG-1999;	99US-0148171.	PR			PR	21			
PR	11-AUG-1999;	99US-0148319.	PR			PR	21			
PR	12-AUG-1999;	99US-0148341.	PR			PR	21			
PR	13-AUG-1999;	99US-0148565.	PR			PR	21			
PR	13-AUG-1999;	99US-0148684.	PR			PR	21			
PR	16-AUG-1999;	99US-0149368.	PR			PR	21			
PR	17-AUG-1999;	99US-0149175.	PR			PR	21			
PR	18-AUG-1999;	99US-0149426.	PR			PR	21			
PR	20-AUG-1999;	99US-0149722.	PR			PR	21			
PR	20-AUG-1999;	99US-0149723.	PR			PR	21			
PR	20-AUG-1999;	99US-0149929.	PR			PR	21			
PR	23-AUG-1999;	99US-0149902.	PR			PR	21			
PR	23-AUG-1999;	99US-0149930.	PR			PR	21			
PR	25-AUG-1999;	99US-0150566.	PR			PR	21			
PR	26-AUG-1999;	99US-0150884.	PR			PR	21			
PR	27-AUG-1999;	99US-0151065.	PR			PR	21			
PR	27-AUG-1999;	99US-0151066.	PR			PR	21			
PR	27-AUG-1999;	99US-0151080.	PR			PR	21			
PR	30-AUG-1999;	99US-0151303.	PR			PR	21			
PR	31-AUG-1999;	99US-0151438.	PR			PR	21			
PR	01-SEP-1999;	99US-0151930.	PR			PR	21			
PR	07-SEP-1999;	99US-0152363.	PR			PR	21			
PR	10-SEP-1999;	99US-0153070.	PR			PR	21			
PR	13-SEP-1999;	99US-0153758.	PR			PR	21			
PR	15-SEP-1999;	99US-0154018.	PR			PR	21			
PR	16-SEP-1999;	99US-0154039.	PR			PR	21			
PR	20-SEP-1999;	99US-0154779.	PR			PR	21			
PR	22-SEP-1999;	99US-0155139.	PR			PR	21			
PR	23-SEP-1999;	99US-0155486.	PR			PR	21			
PR	24-SEP-1999;	99US-0155659.	PR			PR	21			
PR	28-SEP-1999;	99US-0156458.	PR			PR	21			
PR	29-SEP-1999;	99US-0156598.	PR			PR	21			
PR	04-OCT-1999;	99US-0157117.	PR			PR	21			
PR	05-OCT-1999;	99US-0157753.	PR			PR	21			
PR	07-OCT-1999;	99US-0157865.	PR			PR	21			
PR	07-OCT-1999;	99US-0158029.	PR			PR	21			
PR	08-OCT-1999;	99US-0158232.	PR			PR	21			
PR	12-OCT-1999;	99US-0158369.	PR			PR	21			
PR	13-OCT-1999;	99US-0159293.	PR			PR	21			
PR	13-OCT-1999;	99US-0159294.	PR			PR	21			
PR	13-OCT-1999;	99US-0159295.	PR			PR	21			
PR	14-OCT-1999;	99US-0159329.	PR			PR	21			
PR	14-OCT-1999;	99US-0159330.	PR			PR	21			
PR	14-OCT-1999;	99US-0159331.	PR			PR	21			
PR	14-OCT-1999;	99US-0159637.	PR			PR	21			
PR	14-OCT-1999;	99US-0159638.	PR			PR	21			
PR	21-OCT-1999;	99US-0159584.	PR			PR	21			
PR	21-OCT-1999;	99US-0160741.	PR			PR	21			
PR	21-OCT-1999;	99US-0160767.	PR			PR	21			
PR	21-OCT-1999;	99US-0160768.	PR			PR	21			
PR	21-OCT-1999;	99US-0160770.	PR			PR	21			

Alignment Scores:
 Pred. No.: 9.22e-158
 Score: 1588.50
 Percent Similarity: 75.25%
 Best Local Similarity: 60.40%
 Query Match: 59.27%
 DB: 21

US-09-883-797-2 (1-520) x AAC42814 (1-1587)

QY	24	ArgArgLeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeuHis	43
DB	58	AAAAAACTCCCAAACTCTCTTATCGTACGTCTCAAAATATGTAACCTTTACCAT	117
QY	44	AsnSerCysAsnValThrThrLeuPhePheLeuLeuLeuProLeuThrGlyThr	63
DB	118	-----TACCTAATCTCGAATGCGCTCTACATCTCACTACCTCC	156
QY	64	ValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSer	79
DB	157	-----GTCGGCTCTCGCGCAACCTCTCTCTTAGTCTCAGCATCTCACACTC	210
QY	80	TrpSerAsnGlnAlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeu	99
DB	211	TTATACAAACCCACTTCTCAAAATTCCTCTCTCTCTCCACTCTCTCCGCTCTCTCT	270
QY	100	SerPheValLeuThrLeuTyrValAlaAsnArgSerLysProValTyrLeuValAspPhe	119
DB	271	ATCTTTCTAACCCCTCTACTTCTCACAACCTGCTCTCGAGAATCTTTCTCGAATTC	330
QY	120	SerCysTyrLysProGluAspGluArgLysIleSerValAspSerPheLeuThrMetThr	139
DB	331	GCTTGTACAAACCCGACTCTCTCTATATGACACGAAACGTTCTATGGACCGGTCT	390
QY	140	GluGluAsnGlySerPheThrAspThrValGlnPheGlnGlnArgIleSerAsnArg	159
DB	391	CAGCGTGTGCGTATCTTCTCACAAGACACCTCGCTTCCAAACAAAGATCTCGAACGT	450
QY	160	AlaGlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProLysLeu	179
DB	451	TCCGCTCTTGGACAAAGACTTACTTCCCGAGGCTCTTCTAGCTGTCGCGCTATCTCT	510
QY	180	AsnMetSerGluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeu	199
DB	511	TGTATGTCGAAAGCAAGGAAGAGCCGAGCGGTTATGTTGGAGCTATAGACGCACTG	570
QY	200	PheGluLysThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeu	219
DB	571	CTTGAGAAACCGGAGTGAATCTTAAGGATATTGGGATATCTTCTAGCTGTCGCGCTAT	630
QY	220	PheAsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAsp	239
DB	631	TTTAATCCGACGCCCTTCGTTATCGGTATGCTATGCTGAATAATAAAGTCAGAGGAAC	690
QY	240	IleLysSerTyrAsnLeuGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeu	259
DB	691	GTTTTCAGCTATTAACCTTGTGGAATGGTGTGTAGTCTGTCTTATCTCATATGATCTC	750

	Db	1525	AAGTATCCGGTA	1536	
		RESULT	11		
		AAAX23221			
	ID	AAAX23221	standard; DNA; 1611 BP.		
	XX				
	AC	AAAX23221;			
	XX				
	DT	11-JUN-1999	(first entry)		
	XX				
	DE	A. thaliana	EL5 DNA.		
	XX				
	KW	EL5: very long chain fatty acid; VLCFA; beta-keto acyl synthase;			
	KW	plant; vegetable oil; lubricant; fuel; feedstock; plastic; cosmetic;			
	KW	pharmaceutical; edible oil; ss.			
	XX				
	OS	Arabidopsis thaliana.			
	XX				
	PN	WO9854954-A1.			
	XX				
	PD	10-DEC-1998.			
	XX				
	PF	01-JUN-1998;	98WO-US11384.		
	XX				
	PR	03-JUN-1997;	97US-0868373.		
	XX				
	PA	(CRGI) CARGILL INC.			
	PA	(JAWO/) JAWORSKI J G.			
	PA	(POST/) POST-BEITENMILLER MA.			
	PA	(TODD/) TODD J.			
	XX	Jaworski JG, Post-Beitenmiller MA, Todd J;			
	PI				
	XX				
	DR	WPI; 1999-070227/06.			
	XX	P-PSDB; AAW93431.			
	XX				
	PT	New isolated beta-keto acyl synthase polynucleotides - used			
	PT	particularly for the production of transgenic plants having altered			
	PT	levels of very long chain fatty acids in tissues			
	XX				
	PS	Claim 9; Fig 11; 76pp; English.			
	CC	This invention describes the isolation of beta-keto acyl synthase			
	CC	proteins from Arabidopsis thaliana. The products of the invention			
	CC	can be used for producing vegetable oils having elevated levels of			
	CC	very long chain fatty acids (VLCFA) for use as e.g. lubricants, fuels			
	CC	and as a feedstock for plastics, pharmaceuticals and cosmetics. The			
	CC	products can also be used for producing oils having reduced levels of			
	CC	VLCFAs for use as edible oils. This sequence encodes EL5.			
	XX				
	SQ	Sequence 1611 BP; 413 A; 288 C; 382 G; 528 T; 0 other;			
		Alignment Scores:			
		Pred. No.: 1-01e-151 Length: 1611			
		Matches: 1531-50 Matches: 285			
		Percent Similarity: 76.20% Conservative: 96			
		Best Local Similarity: 57.00% Mismatches: 104			
		Query Match: 57.15% Indels: 15			
		Gaps: 20			
		DB:			
		US-09-883-797-2 (1-520) x AAAX23221 (1-1611)			
	QY	23 ArgArgArgLeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeu	42		
	Db	139 AGACGAAGCTTCCTAATTCTTTACAAGCGCTCAACATGAATACTGCAAGTAGGTAT	198		
	QY	43 HisAsnSerCysAsnValThrThrIleLeuPhePheLeuIleLeuProLeuThrGly	62		
	Db	199 CAT-----TACCCTCATCTACTCTCTCAAGCTCTCTTGTTGGTTCATTAATGCCG	249		
	QY	63 ThrValLeuValGlnLeuLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrpSerAsn	82		
	Db	250 GTTTTAGTCACAGAGATCTCTCGGATTAAACAACAGAGATCTTACCAGATTGG-----	303		

Alignment Scores:

Pred. No.:	1.25e-151	Length:	1853
Score:	1531.50	Matches:	285
Percent Similarity:	76.20%	Conservative:	96
Best Local Similarity:	57.00%	Mismatches:	104
Query Match:	57.15%	Indels:	15
DB:	21	Gaps:	4

US-09-883-797-2 (1-520) x AAC50224 (1-1853)

QY	23	ArgArgArgLeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeu	42
DB	230	AGAGGAAGCTTCCTAATTTCTTACAAACGCTCAACATGAAATACGTAAGCTAGTTAT	289
QY	43	HisAsnSerCysAsnValThrThrThrLeuLeuPhePheLeuLeuLeuLeuProLeuThrGly	62
DB	290	CAT-----TACCTCATTTACTCATCTCTTCAAGCTCTGTTTGGTTCCTCAATTAATGCGG	340
QY	63	ThrValLeuValGlnLeuLeuThrThrPheAspThrPheSerGluLeuTyrSerAsn	82
DB	341	GTTTTGTCTACAGAGATCTCTCGATTAAACAACAGACGATCTTTACAGATTGG-----	394
QY	83	GlnAlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSer-----	100
DB	395	-----CTTCATCTCCAATACATCTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	442
QY	101	-----PheValLeuThrLeuThrValAlaAsnArgSerLysProValTyrLeuValAsp	118
DB	443	GCTATCTTTGGCTCCACCGTTTACATCATGAGTGTCCAGATCTGTTTATCTCTGTTGAT	502
QY	119	PheSerCysTyrLysProGluAspGluArgLysLysSerValAspSerPheLeuThrMet	138
DB	503	TACTCTGTATCTCTCCGGAGAGTCTTCAGGTAAAGTATCAGAAAGTTATGATCAT	562
QY	139	ThrGluGluAsnGlySerPheThrAspAspThrValGlnPheGlnGlnArgLysSerAsn	158
DB	563	TCTAAGTTGATTGAAGATTTCATGAGTCATCTTTAGAGTTTCAGAGAAAGATTCTTGAA	622
QY	159	ArgAlaGlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerProProLys	178
DB	623	CGTTCGGTTTAGGAAAGAGACTTATCTCCCTGAAGCTTTTACATTTGATCTCCCTCCGAGG	682
QY	179	LeuAsnMetSerGluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSer	198
DB	683	CCTACGATGATCGCGCTCGTGAGGAATCTGACGAGTAATGTTGGTCTCTTGATAAG	742
QY	199	PhePheGlyLysThrGlyIleLysProAlaGluValGlyIleLeuLeuValAsnCysSer	218
DB	743	CTTTTCGAGAATACCAAGATTAAACCTTAGGATATTTGGTGTGTTGTTGTAATTGTAGC	802
QY	219	LeuPheAsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGlu	238
DB	803	TTGTTTAAATCCACACCTCGTTGTCAGCTATGATTGTTTAAACAGTAAAGCTTAGAGG	862
QY	239	AspIleLysSerTyrAsnLeuGlyMetGlyCysSerAlaGlyLeuIleSerIleAsp	258
DB	863	AATGTTAAGATTCTTAACCTTGGTGAATTTAGTGTGTTGTTGTTTATCTATCGAT	922
QY	259	LeuAlaAsnAsnLeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGlu	278
DB	923	TTAGCTAAGATATGTTCAAGTTCATAGGAATACCTTATGCTGTTGTTGTTAGTCTAG	982
QY	279	AsnIleThrLeuAsnThrTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIle	298
DB	983	AACATTACTCAGAATTGTTATTTTGGGAATAAGAGGCTATGTTGATCCCAATTTGTTG	1042
QY	299	PheArgMetGlyAlaAlaIleLeuLeuSerAsnArgArgGlnAspArgLysLysSer	318
DB	1043	TTTCGGTGTGTTGTCGGGATTTCTTGTGCAACAGGGGAAAGATCGTAGACGGTCT	1102
QY	319	LysTyrSerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsn	338
DB	1103	AAGTATAAGCTTGTTCATACCGTTAGGACTCATAAAGAGCTGTTGAGAGGCTTTCAAC	1162

QY	339	CysValTyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeu	358
DB	1163	TGTTTACCAGAGCAAGATGATAATGGGAGACCGGGTTTCGTTGTCGAAGATCTT	1222
QY	359	MetSerValAlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeu	378
DB	1223	ATGGCTATAGCTGGGAGAGCTCTTAAGCGGAATATACCTACTTCTAGGCTCTTGGTCTT	1282
QY	379	ProLeuSerGluGlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeu	398
DB	1283	CCTAATAGTCAGCAGATCTCTGTTTTCATGACTTTGGTTACGAAGAACTGTTTAACTCG	1342
QY	399	LysValLysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAla	418
DB	1343	AACTGAAGCGGTATATTCGGATTCAAGCTTGGTGTGATCATTTCTGTATCATCATGCT	1402
QY	419	GlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTyrHisMet	438
DB	1403	GSTGGTAGAGCTGTGATTGATGAGCTTGAGAAGAACTCTGCAGCTTCCACACTCATGTC	1462
QY	439	GluProSerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTyr	458
DB	1463	GAGGATCCAGAAATGACACTGCACAGATTTGGAACACTTCTTCGAGCTCGATTGGTAT	1522
QY	459	GluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTyrGlnIle	478
DB	1523	GAACCTGCTTACATAGAGGCTAAAGGTAGGATGAAGAAAGAAACCGGTTTGGCAGATT	1582
QY	479	AlaPheGlySerGlyPheLysCysAsnSerAlaValTyrLysAlaLeuArgProValSer	498
DB	1583	GCTTTTGAAGTGGGTTTAAAGTAAACAGTGCAGTTTGGTGGTCTTAAACAATGTC---	1639
QY	499	ThrGluGluMetThrGlyAsnAlaTyrAlaGlySerIleAspGlnTyrProValLysVal	518
DB	1640	---AAGCCTCTCGTTAGTAGTCGTCGGGAACACTGCATCCGATATCCGGTTAAGCTC	1696
RESULT	13		
AAAT04124			
ID	AAAT04124	standard; cDNA to mRNA; 1783 BP.	
XX	AAAT04124;		
AC	AAAT04124;		
XX	XX		
DT	16-JAN-1996 (first entry)		
XX	XX		
DE	Jojoba wax-synthase cDNA clone pcn7614.		
XX	XX		
KW	Wax-synthase; long-chain alcohol-fatty-acyl-transferase; wax ester;		
KW	Jojoba; oilseed; transgenic plant; crop improvement; Brassica; ds.		
OS	Simmondsia chinensis.		
XX	XX		
PH	Key	Location/Qualifiers	
FT	CDS	10..1575	
FT		/*tag= a	
FT		/EC_number= 2.3.1.75	
XX	US5445947-A.		
PN	XX		
PD	29-AUG-1995.		
XX	XX		
PF	20-NOV-1991; 91US-0796256.		
XX	XX		
PR	20-MAY-1993; 93US-0066299.		
PR	20-NOV-1991; 91US-0796256.		
PR	21-AUG-1992; 92US-0933411.		
PR	13-NOV-1992; 92WO-0509863.		
XX	XX		
PA	(CALJ) CALGENE INC.		
XX	XX		
PI	Lardizabal KD, Lassner MW, Metz JG;		
XX	XX		
DR	WPI; 1995-310894/40.		

PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 23-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 25-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151330.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
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 PR 14-OCT-1999; 99US-0159329.
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 PR 14-OCT-1999; 99US-0159331.
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 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
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 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
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 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161922.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Alignment Scores:
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 QY 73 PheAspThrPheSerGluLeuTyrSerAsnGlnAlaValGlnLeuLeuAspThrAlaThrArg 92
 Db 352 CCAGATGATCTCAAAACAGCTCTGGATCCAT-----CTACAATCAATCTGGTTAGATC 405
 QY 93 LeuThrCysLeuValPheLeuSerPheValLeuThrLeuTyrValAlaAsnArgSerLys 112
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 QY 193 PheGlyAlaLeuAspSerLeuPheGluLysThrGlyIleLysProAlaGluValGlyIle 212
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Thu Feb 20 11:03:34 2003

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Job time : 342 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 10:27:18 : Search time 131 Seconds
(without alignments)
2021.743 Million cell updates/sec

Title: US-09-883-797-2

Perfect score: 2680

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Searched:

424239 seqs, 254661826 residues

Total number of hits satisfying chosen parameters: 848478

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications_NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1639	61.2	1530	9	US-09-938-842A-1205	Sequence 1552, Ap
4	1588.5	59.3	1587	9	US-09-938-842A-1598	Sequence 1205, Ap

5	1563	58.3	1548	10	US-09-883-797-13	Sequence 13, Appl
6	1531.5	57.1	1611	10	US-09-883-797-9	Sequence 9, Appli
7	1441	53.8	1650	10	US-09-883-797-7	Sequence 7, Appli
8	1438.5	53.7	1491	10	US-09-892-325-3	Sequence 3, Appli
9	1438.5	53.7	1494	9	US-09-938-842A-569	Sequence 569, App
10	1438.5	53.7	1502	10	US-09-883-797-11	Sequence 11, Appl
11	1438.5	53.7	1807	10	US-09-892-325-2	Sequence 2, Appli
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15	1317.5	49.2	1521	10	US-09-877-476-37	Sequence 37, Appl
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19	1308.5	48.8	1521	10	US-09-877-476-39	Sequence 39, Appl
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24	1302.5	48.6	1521	10	US-09-877-476-19	Sequence 19, Appl
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26	1301.5	48.6	1521	10	US-09-877-476-25	Sequence 25, Appl
27	1300.5	48.5	1521	10	US-09-877-476-13	Sequence 13, Appl
28	1300	48.5	1518	10	US-09-877-476-17	Sequence 17, Appl
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30	1299.5	48.5	1524	10	US-09-877-476-3	Sequence 3, Appli
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32	1298	48.4	1479	10	US-09-877-476-27	Sequence 27, Appl
33	1296.5	48.4	1521	10	US-09-877-476-11	Sequence 11, Appl
34	1295.5	48.3	1521	10	US-09-877-476-29	Sequence 29, Appl
35	1295.5	48.3	1521	10	US-09-877-476-5	Sequence 5, Appli
36	1294	48.3	1736	10	US-09-877-476-9	Sequence 9, Appli
37	1293	48.2	1518	10	US-09-877-476-9	Sequence 1987, Ap
38	958	35.7	1431	9	US-09-938-842A-1987	Sequence 774, App
39	528.5	19.7	811	10	US-09-770-445-774	Sequence 4051, App
40	501	18.7	409	10	US-09-878-574-4051	Sequence 253, App
41	460	17.2	468	10	US-09-770-444-253	Sequence 1065, App
42	427	15.9	387	10	US-09-878-574-1065	Sequence 2604, Ap
43	301	11.2	343	10	US-09-878-574-2604	Sequence 12488, A
44	295	11.0	276	10	US-09-837-654-2	Sequence 2, Appli
45	160	6.0	1359	10		

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09883797
; Patent No. US20020066123A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beittemiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/09/883,797
; CURRENT FILING DATE: 2001-06-18
; PRIOR FILING DATE: 08/868,373
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-883-797-1

Alignment Scores:
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Length: 1560
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Matches: 520
Best Local Similarity: 100.00%
Conservative: 0
Query Match: 100.00%
Mismatch: 0
Indels: 0

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RESULT 2

US-09-938-842A-1552

; Sequence 1552, Application US/09938842A

; Patent No. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAIN

; FILE REFERENCE: SAME, AND METHODS OF USE

; CURRENT APPLICATION NUMBER: US/09/938,842A

; PRIOR FILING DATE: 2001-08-24

; PRIOR FILING DATE: 2001-08-24

; PRIOR FILING DATE: 2001-08-24

; PRIOR FILING DATE: 2001-01-16

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 1552

; LENGTH: 1563

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; US-09-938-842A-1552

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Score: 2680.00 Matches: 520

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

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 QY 201 GluLysThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPhe 220
 Db 601 GAGAAACCGGAATTAACCGCGGAAAGTCGGAATCTTGATTAACCTGACGTTATTC 660
 QY 221 AsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIle 240
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 QY 321 SerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysVal 340
 Db 961 TCGCTGCTCAACGCTGTTGGAACACATAAAGGATCAGACGACAGAACTACAATTCGCTG 1020
 QY 341 TyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSer 360
 Db 1021 TACCAAGAGGAGACGAGAGGAGCAATCGGTGCTCTTTAGCTAGAGAGCTCATGCTCT 1080
 QY 361 ValAlaGlyAspAlaLeuLysThrAsnIleThrLeuGlyProMetValLeuProLeu 380

Db 1081 GTCCCGGACACCTCTGAAACAAACATCACGACTTTAGGACCGATGTTCTTCATTG 1140
 QY 381 SerGluGlnLeuMetPheLeuIleSerLeuValLysArgTysMetPheLysLeuLysVal 400
 Db 1141 TCAGACAGTGTGATGTTCTTGTATTCCTTGGTCAAAAGAGATGTTCAAGTTAAAGTT 1200
 QY 401 LysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGly 420
 Db 1201 AAACCGTATATTCGGATTTCAAGCTAGCTTTTCGAGCATTTCTGTATTCAGCAGAGGT 1260
 QY 421 ArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTyrPheHisMetGluPro 440
 Db 1261 AGAGCGGTTCTAGCAAGTGCAGAGAAATCTTGATCTCAAGATTTGGCAGATGCAACCT 1320
 QY 441 SerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTyrTrpGluMet 460
 Db 1321 TCTAGAACTACCTTGCACAGATTTGGTAACACTTCAGTAGTACGCTTGTGTATGAGATG 1380
 QY 461 AlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPhe 480
 Db 1381 GCTTATACCGAAGCTAAGGTCGGGTTAAAGCTGGTGACCGACTTTGGCAGATTCGCTTT 1440
 QY 481 GlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGlu 500
 Db 1441 GATCGGGTTTCAAGTGTAAATAGTGGGTTTGAAAGCGTTACGACCGGTTTCGACGGAG 1500
 QY 501 GluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysValValGln 520
 Db 1501 GAGATGACCGGTAATGCTTGGCTGGTTCGATTGATCAATAATCCGGTTAAAGTTGTCAA 1560

RESULT 3

US-09-938-842A-1205
 ; Sequence 1205, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SAME, AND METHODS OF USE
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 1205
 ; LENGTH: 1530
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-1205

Alignment Scores:

Pred. No.: 1,25e-187 Length: 1530
 Score: 1639.00 Matches: 304
 Percent Similarity: 78.38% Conservative: 84
 Best Local Similarity: 61.41% Mismatches: 101
 Query Match: 61.16% Indels: 6
 DB: Gaps: 3

US-09-883-797-2 (1-520) x US-09-938-842A-1205 (1-1530)

QY 24 ArgArgLeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeuHis 43
 Db 43 CGTATCTACCTGATTTCAAAAATCAGTGAAGCTTAAATATGTGAAGCTTGGTTACCAT 102
 QY 44 AsnSerCysAsnValThrThrIleLeuPhePheLeuIleLeuProLeuThrGlyThr 63


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QY 100 SerPheValLeuThrLeuValAlaAsnArgSerLysProValTyrLeuValAspPhe 119
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 271 ATCTTCTAACACCTCTACTTCAACACTCGTCCCTCGAGAAATCTTCTCTCGATTTC 330

QY 120 SerCysTyrLysProGluAspGluArgLysIleSerValAspSerPheLeuThrMetThr 139
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 331 GCTTGTACAAACCGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 390

QY 140 GluGluAsnGlySerPheThrAspThrValGlnPheGlnGlnArgIleSerAsnArg 159
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 391 CAGCGTGTCTGATCTCTCACAGAGACACCTCGCTTCTCCACAAAGATCTCTCGAACGT 450

QY 160 AlaGlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProLysLeu 179
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 451 TCCGCTCTTGACAAAGACTTACTTCCCGAGGCTCTTACTGTCCTCGCTCTCTCTCTCT 510

QY 180 AsnMetSerGluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeu 199
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 511 TGTATGCTGAAGCAAGGAAAGAGCCGAGCGGTATGTTTGGAGCTATACACCGAGTG 570

QY 200 PheGlyThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeu 219
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 571 CTTGAGAAACCGGAGTGAATCTTAAGGATATTGGGATCTTGTCTGTAATTTGATCTTG 630

QY 220 PheAsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAsp 239
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 631 TTTAATCCGAGCGCTCTGTTATCGCTATGATCGTGAATAATAATAAGCTCAGAGGAAC 690

QY 240 IleLysSerTyrAsnLeuGlyMetClyCysSerAlaGlyLeuIleSerIleAspLeu 259
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 691 GTTTTGAGCTATAACCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 750

QY 260 AlaAsnLeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrClnAsn 279
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 751 GCTAAACAGCTCTTTCAGGTTCAACCAATTCATATCCACTAGTAGTGAGCAGCAGAAC 810

QY 280 IleThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnIlePhe 299
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 811 ATACCTTAACCTGGTATTAGGCAACGACGACGATCAATGCTCTCTCAAACTGCATCTTC 870

QY 300 ArgMetGlyGlyAlaAlaIleLeuLeuSerAsnArgGlnAspArgLysLysSerLys 319
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 871 CGAATGGTGGCGCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 930

QY 320 TyrSerLeuValAsnValValArgThrHisLysGlySerAspLysAsnTyrAsnCys 339
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 931 TACCAACTCATCCACACCTCCGTACACACAAAGGATCTGACGACACGCTTAACTGTC 990

QY 340 ValTyrGlnLysGlu-----AspGluArgGlyThrIleGlyValSerLeuAlaArgGlu 357
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 991 GTTTACCAACGGGACACACGACGACACAAACAATCGGTCTCTCACTTTCCAAAAAC 1050

QY 358 LeuMetSerValAlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetVal 377
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1051 CTAATGGGTATAGCTGGAGAGCTCTCAAGACGAAACATAACACCTCTGGGACCGCTAGTT 1110

QY 378 LeuProLeuSerGluClnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLys 397
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1111 CTACCAATGCTGAACACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1170

QY 398 Leu---LysValLysProTyrIleProAspPheLysLeuAlaPheLysIle 416
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1171 GTGAAGAAATAAAACCTTATCTCTGATTTCAAGTAGCTTTTCGAGCACTCTGCAATC 1230

QY 417 HisAlaGlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLysAspTrp 436
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1231 CACCGGAGGACAGCAGTCTCGATGAGATTGAGAGAAATTTGGATTATCTGAGTGG 1290

QY 437 HisMetGluProSerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeu 456
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1291 CATATGGAACCTTCGAGATGACCTTTGAACCGGTTTGGAAATACTTTCAGTAGCTCGCTT 1350
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QY 457 TrpTyrGluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrp 476
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1351 TGGTATGAGCTTGGCTATAGTAGGCTAAAGGAAGGATTAAAGAGAGGATAGGACTTGG 1410

QY 477 GlnIleAlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArg--- 495
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1411 CAGATTGCTTTTGGATCCGGTTTTAAGTCTAATAGTTCGGTTTGGAGAGCTTTGGAAC 1470

QY 496 -----ProValSerThrGluGluMetThrGlyAsnAlaTrpAlaGlySerIleAspGln 513
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1471 ATCCATCCGTCACAGGAGGAAGAAAGAAAGACTAATCTCTGGATTGATGAGATTCATGAG 1530

QY 514 TyrProValLysVal 518
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1531 TTTCCCGCTGCCGGTT 1545

RESULT 5
US-09-883-797-13
; Sequence 13, Application US/09883797
; Patent No. US20020066123A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beittemiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/09/883,797
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 08/868,373
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-883-797-13

Alignment Scores:
Pred. No.: 1.86e-178 Length: 1548
Score: 1563.00 Matches: 293
Percent Similarity: 76.39% Conservatives: 92
Best Local Similarity: 58.13% Mismatches: 111
Query Match: 58.32% Indels: 8
DB: 10 Gaps: 4

US-09-883-797-2 (1-520) x US-09-883-797-13 (1-1548)
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QY 14 AspSerSerSerAlaVal---IleArgIleArgArgLeuProAspLeuThrSer 32
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 46 GATGGTCTCTGGAGTTCAGATCCGACAAACACCGGATGCTACCGGATTTTCTCCAGAC 105

QY 33 ValLysLeuLysTyrValLysLeuGlyLeuHisAsnSerCysAsnValThrIleLeu 52
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 106 GTGAATCTCAAGTAGTGTGAATTTAGTTTACCAT-----TACTTAATCTCAATCTC 156

QY 53 PhePheLeuIleLeuLeuProLeuThrGlyThrValLeuValGlnLeuThrGlyLeuThr 72
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 157 TTGACTCTCTGTTTATTCCTCCCTCGCGCTGTTATCTCTCGTGAAGCCCTCAGATGAAC 216

QY 73 PheAspThrPheSerGluLeuTrpSerAsnGlnAlaValGlnLeuAspThrAlaThrArg 92
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 217 CCAGATCATCTCAAAACAGCTCTGGATCCAT-----CTACAATACAATCTGGTTAGTATC 270

QY 93 LeuThrCysLeuValPheLeuSerPheValLeuThrLeuThrValAlaAsnArgSerLys 112
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 271 ATCATCTGTTCAGCGATTTCTAGTCTTCGGGTTAACGGTTTATGTTATCACCGGACCTAGA 330

QY 113 ProValTyrLeuValAspPheSerCysTyrLysProGluAspGluArgLysIleSerVal 132
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 331 CCGGTTTACTTGGTTGATTTCTCTGTGTTATCTCCCACTGATCATCTCAAAAGCTCCTTAC 390

QY 133 AspSerPheLeuThrMetThrGluGluAsnGlySerPheThrAspThrValGlnPhe 152
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Db 1471 GCATTAAGCATGTG-----AAACCTTGAACAACAGCTCCTTGGGAAGATTGTATTGAC 1524

Qy 513 GlnTyrProVal 516
Db 1525 AAGTATCCGGTA 1536
RESULT 6
US-09-883-797-9
; Sequence 9, Application US/09883797
; Patent No. US20020066123A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beittemmiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/09/883,797
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 08/868,373
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1611
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-883-797-9
Alignment Scores:
Pred. No.: 1,25e-174 Length: 1611
Score: 1531.50 Matches: 285
Percent Similarity: 76.20% Conservative: 96
Best Local Similarity: 57.00% Mismatches: 104
Query Match: 57.15% Indels: 15
DB: 4 Gaps: 4
US-09-883-797-2 (1-520) x US-09-883-797-9 (1-1611)
Qy 23 ArgArgArgLeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeu 42
Db 139 AGACGAAGCTTCTCTATTTCTTACAAGCGTCAACATGAATACGTACAGTAGTTAT 198
Qy 43 HisAsnSerCysAsnValThrIleLeuPhePheLeuIleLeuProLeuThrGly 62
Db 199 CAT-----TACCTCATTTACTCATCTCTCAAGCTCTCTTTGGTTCCATTAATGCGG 249
Qy 63 ThrValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrpSerAsn 82
Db 250 GTTTTACTCAGAGATCTCTCGATTAAACACAGACAGATCTTACAGATTGG----- 303
Qy 83 GlnAlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSer----- 100
Db 304 -----CTTCATCTCCAATACAATCTCGTTGCTTCTTCTCTCTCTCTCTCTT 351
Qy 101 -----PheValLeuThrLeuTyrValAlaAsnArgSerLysProValTyrLeuValAsp 118
Db 352 GCTATCTTTGGCTCCACCGCTTATCATCATGCTCCAGATCTGTTTATCTCGTTGAT 411
Qy 119 PheSerCysTyrLysProGluAspGluArgLysIleSerValAspSerPheLeuThrMet 138
Db 412 TACTCTTGTATCTCTCCCGGAGATCTTCAGTTTAAAGTATCAGAGAAAGATTATGGATCAT 471
Qy 139 ThrGluGluAsnGlySerPheThrAspAspThrValGlnPheGlnGlnArgIleSerAsn 158
Db 472 TCTAAGTTGATTGAAGATTTCATGAGTCATCTTTAGAGTTTTCAGAGAAAGATTCTTGAA 531
Qy 159 ArgAlaGlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProLys 178
Db 532 CGTTCTGTTTGAAGAGAGAGACTTATCTCCCTGAAGCATTACATCTATCCCTCCGAGG 591
Qy 179 LeuAsnMetSerGluAlaArgAlaGluAlaValMetPheGlyAlaLeuAspSer 198
Db 592 CCTACGATGATGCGGCTCGTGAGGAATCTGAGCAGGTAATGTTTGTGCTCTTGTATAAG 651

Db 391 GCTCGTTTCATGGACATCTAGACTCACCAGAGATTTCGATGACTCTCTCTCGAGTTT 450
Qy 153 GlnGlnArgIleSerAsnArgAlaGlyLeuGlyAspGluThrTyrLeuProArgGlyIle 172
Db 451 CAACGCAAGATCCTTGGAGCTTCTGTTTAGGGAAGACACTATATCCCTGAAGCTATG 510
Qy 173 ThrSerThrProLysLeuAsnMetSerGluAlaArgAlaGluAlaValMet 192
Db 511 CATTAATGTTCCACCAGAAATTTCAATGCTGCTGCTAGAGAAAGCTGAACAAGTCATG 570
Qy 193 PheGlyAlaLeuAspSerLeuPheGluLysThrGlyIleLysProAlaGluValGlyIle 212
Db 571 TTTGGTCTTTAGATAACCTTTTCGCTAACACTAATGTGAACCAAGGATATTGGAATC 630
Qy 213 LeuIleValAsnCysSerLeuPheAsnProThrProSerLeuSerAlaMetIleValAsn 232
Db 631 CTGTGTGTAATGTAGTCTCTTAAATCCAACCTCCCTGCTTCTGCAATGATGTGAAC 690
Qy 233 HisTyrLysMetArgGluAspIleLysSerTyrAsnLeuGlyMetGlyCysSerAla 252
Db 691 AAGTATAGCTTASAGGTACATTAGAGCTACAATCTAGCGGTATGGTTGCGAGCGG 750
Qy 253 GlyLeuIleSerLeuAspLeuAlaAsnAsnLeuLeuLysAlaAsnProAsnSerTyrAla 272
Db 751 GGAGTTATCTGCTGATCTTGTAAAGACATGTTGTGTCATAGAACACATTATGCG 810
Qy 273 ValValValSerThrGluAsnIleThrLeuAsnTrpTyrPheGlyAsnAspArgSerMet 292
Db 811 GTTGTGTTTCTACTGAGACATTTACTCAGATTTGTTGTTGTTTAAACAAAGATTCGATG 870
Qy 293 LeuLeuCysAsnCysIlePheArgMetGlyAlaAlaIleLeuLeuSerAsnArgArg 312
Db 871 TTGATACCGAACTGCTTGTTCGAGTTGGTGGCTCTGCGGTTTGTCTATCGAACAGTCG 930
Qy 313 GlnAspArgLysLysSerLysTyrSerLeuValAsnValAlaArgThrHisLysGlySer 332
Db 931 AGGACAAGAGACGGCTTAAGTACAGCTTCTACATGTTAGTCAGGACTCACCGTGGAGCA 990
Qy 333 AspAspLysAsnTyrAsnCysValTyrGlnLysGluAspGluArgGlyThrIleGlyVal 352
Db 991 GATGATAAGCTTTCCTGTTTATCAAGACAGGATGATACAGGGGAAGACCGGGTT 1050
Qy 353 SerLeuAlaArgGluLeuMetSerValAlaGlyAspAlaLeuLysThrAsnIleThrThr 372
Db 1051 TCGTTGTGGAAGATCTAATGCGGATTCGAGGGAACTCTCAAAACCAATATCACTACA 1110
Qy 373 LeuGlyProMetValLeuProLeuSerGluGlnLeuMetPheLeuIleSerLeuValLys 392
Db 1111 TTGGTCTCTTGTCTACCGATAAGTGAGCAGATCTCTTCTTATGACTTAGTTGTCG 1170
Qy 393 ArgLysMetPheLysLeuLysValLysProTyrIleProAspPheLysLeuAlaPheGlu 412
Db 1171 AAGAAGCTCTTTAACGGTAAAGTGAACCGTATATCCCGATTTCAAACTGCTTTCGAG 1230
Qy 413 HisPheCysIleHisAlaGlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAsp 432
Db 1231 CATTTCTGATCATCTGCTGGTGAAGAGCTGTGATCGATGAGTAGAAGAATCTGCGAG 1290
Qy 433 LeuLysAspTrpHisMetGluProSerArgMetThrLeuHisArgPheGlyAsnThrSer 452
Db 1291 CTTTCCACAGTTCATGCGAGGCTTCGAGATGACTCTTCATCGATTGTTGTAACACATCT 1350
Qy 453 SerSerSerLeuTrpTyrGluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGly 472
Db 1351 TCGAGCTCCATTTGGTATGATTTGCTTACATTTGAAGCGAAGGAGGATCGGAAGAGT 1410
Qy 473 AspArgLeuTrpGlnIleAlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLys 492
Db 1411 AATCGTGTGTGGCAATTCGGGTTTCGGAAGTGGATTTAAATGTAATAGCCGATTTGGAA 1470
Qy 493 AlaLeuArgProValSerThrGluGluMetThrGlyAsnAlaTrpAlaGlySerIleAsp 512

QY 163 GlyAspGluThrTyrLeuProArgGlyIleThrSerThrProProLysLeuAsnMetSer 182
 DB 412 GGTGAGGAGACTGTCTCCCTCCGCTATTTCATTATATATTCCTCCACACCAACATCGGAC 471
 QY 183 GluAlaArgAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLys 202
 DB 472 GCGGCTAGAGCGGCTCAGATGGTTATCTTCGAGGCCATGACGATCTTTTCAGAAA 531
 QY 203 ThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnPro 222
 DB 532 ACCGGTCTTAACCTTAAGACCTGACATCCCTATCTGTCACCTGCTCTCTCTCTCTCC 591
 QY 223 ThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSer 242
 DB 592 ACACCATCGCTCAGCTATGGTCATCAACAATAAAGCTTAGGAGTAATATCAAGAGC 651
 QY 243 TyrAsnLeuGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAsn 262
 DB 652 TTCAATCTTTGGGGATGGGTGACGGCGGCTGATCTCAGTTGATCTAGCCCGGAC 711
 QY 263 LeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeu 282
 DB 712 TTGCTCCAGTTCATCCCAATTCAAATGCAATCATCTGTCAGACCGGATCATACGCCCT 771
 QY 283 AsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGly 302
 DB 772 AATTACTATCAAGCAACGAGAGCCATGTGTACCAATGTCTCTCCGATGGGT 831
 QY 303 GlyAlaIleLeuLeuSerAsnArgArgGlnAspArgLysLysSerLysTyrSerLeu 322
 DB 832 GCGGACGCCATACATGTCAAACCGCGGTCTGACCGGTGCGGACCAATACAAAGCTT 891
 QY 323 ValAsnValValArgThrHisLysGlySerAspLysAsnTyrAsnCysValTyrGln 342
 DB 892 TCCACCTGCTCCGGACACACCGTGGCGCTGACGAAAGTCTTCTACTGTGTCTACGAA 951
 QY 343 LysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAla 362
 DB 952 CAGGAAGACAAAGAGACAGCTGGCATCAACTGTGTCACCAAGATCTCATGGCCATCGCC 1011
 QY 363 GlyAspAlaLeuLysThrAsnIleThrLeuGlyProMetValLeuProLeuSerGlu 382
 DB 1012 GGTGAAGCCCTCAAGGCAACATCACCACAATAGTCTCTTGGTCTACCGGCGTCAGAA 1071
 QY 383 GlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysValLysPro 402
 DB 1072 CAACTTCTCTCTCAGCTCCCTAATCGGAGCTAAATCTTCAACCCGAAATGGAAACCA 1131
 QY 403 TyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyArgAla 422
 DB 1132 TACATACGGATTTCAAGCTGGCTTCCGACACATTTGTCATTCACGCGAGGAGGACGG 1191
 QY 423 ValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArg 442
 DB 1192 GTATCGACGAGCTCCAAAAGAAATCTCAACTATCAGAGAACACGTTGAGGCGCTCAAGA 1251
 QY 443 MetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTrpTyrGluMetAlaTyr 462
 DB 1252 ATGACACTACATCGTTTGTGTAACACGCTCATCTTCATGTTATGTTAGGAGCTTAGCTAC 1311
 QY 463 ThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySer 482
 DB 1312 ATCGAGTCTAAAGGAGAAATGAGGAGGCGATCGCGTTTGGCAAAATCGCGTTTGGGAGT 1371
 QY 483 GlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMet 502
 DB 1372 GGTTCAGAGTCAACTCTCGCGGTGGAAATGTAACTACGATTAAGACACACCTTAAG --- 1428
 QY 503 ThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProVal 516
 DB 1429 ---GACGGACCACTGGTCCGATTGATCGACCGTTACCTGTC 1467

RESULT 9

US-09-938-842A-569
 : Sequence 569, Application US/09938842A
 : Patent No. US20020160378A1
 : GENERAL INFORMATION:
 : APPLICANT: Harper, Jeff
 : APPLICANT: Kreps, Joel
 : APPLICANT: Wang, Xun
 : APPLICANT: Zhu, Tong

: TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAIN
 : FILE REFERENCE: SCRIPL300-3
 : CURRENT APPLICATION NUMBER: US/09/938,842A
 : PRIOR FILING DATE: 2001-08-24
 : PRIOR APPLICATION NUMBER: US 60/227,866
 : PRIOR FILING DATE: 2000-08-24
 : PRIOR APPLICATION NUMBER: US 60/264,647
 : PRIOR FILING DATE: 2001-01-16
 : PRIOR APPLICATION NUMBER: US 60/300,111
 : PRIOR FILING DATE: 2001-06-22
 : NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 569

LENGTH: 1494

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-938-842A-569

Alignment Scores:

Pred. No.:	1-8e-163	Length:	1494
Score:	1438.50	Matches:	279
Percent Similarity:	74.49%	Conservative:	89
Best Local Similarity:	56.48%	Mismatches:	113
Query Match:	53.68%	Indels:	13
DB:	9	Gaps:	6

US-09-883-797-2 (1-520) x US-09-938-842A-569 (1-1494)

QY 26 LeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeuHisAsnSer 45
 DB 16 ATCCGAGGTTCTAGCTCGTGAAGCTCAAGTACGTGAACCTTGGTTACCAATATTG 75
 QY 46 CysAsnValThrIleLeuPhePheIleLeuProLeuThrGlyThrValLeu 65
 DB 76 GTTAAC-----CATTCCTTGAGTTTCTTTTGATC---CCGATCATGGCTATTGTCGCC 126
 QY 66 ValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrpSerAsnGlnAlaVal 85
 DB 127 GTGAGCTTCTTCGGATGGGTCTGGAAGAGATCCTTAATGTTGGAAT-----TCACCTC 180
 QY 86 GlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeuThrLeu 105
 DB 181 CAGTTTGACCTAGTTCAGGTTCTATGTTCTTCCTTCCTTCATCTTCATCTCCACTGTT 240
 QY 106 TyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysProGlu 125
 DB 241 TACTTCATGTCACGACCGACCATCTACCTCGTTGACTATCTTGTGTACAGCCACT 300
 QY 126 AspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPhe 145
 DB 301 GTCAGGTGTCGTGTC-----CCCTTCGCACTTTTCATGGAACACTCTCGTTTGATC 351
 QY 146 ThrAspAsp-----ThrValGlnPheGlnArgIleSerAsnArgAlaGlyLeu 162
 DB 352 CTCAGGACACAGCCTAAGAGCGTCGAGTCCAAATGGAATCCTTGAACGTTCTGGGCTC 411
 QY 163 GlyAspGluThrTyrLeuProArgGlyIleThrSerThrProProLysLeuAsnMetSer 182
 DB 412 GGTGAGGAGACTGTCTCCCTCCGGCTATTTCATTATATTCTCCACCAACCACTGGAC 471
 QY 183 GluAlaArgAlaGluAlaGluAlaMetPheGlyAlaLeuAspSerLeuPheGluLys 202
 DB 472 GCGGCTAGAGGAGGCTCAGATGGTTATCTTCGAGGCCATGGACGATCTTTTCAAGAAA 531

CONTAIN

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QY 203 ThrGlyIleLysProAlaGluValcIlyIleLeuIleValAsnCysSerLeuPheAsnPro 222
Db 532 ACCGGTCTTAAACCTAAAGAGCTCGACATCTTATCGCAACTGCTCTCTTCTCTCC 591
QY 223 ThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSer 242
Db 592 ACACCATCGCTCTCAGCTATGTCATCAACAATAATAGCTTAGGAGTAAATATCAAGAGC 651
QY 243 TyrAsnLeuGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAsn 262
Db 652 TTCAATCTTTCCGGGATGGGTGAGCGCGGCGCTGATCTCAGTTGATCTAGCCGCGAC 711
QY 263 LeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeu 282
Db 712 TTGCTCCAGTTCATCCCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 771
QY 283 AsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGly 302
Db 772 AATTACTATCAAGGACGAGAGCCATGTTGTTACCCAAATGTTCTCTCCGCGATGGGT 831
QY 303 GlyAlaLalleLeuLeuSerAsnArgArgGlnAspArgLysLysSerLysTyrSerLeu 322
Db 832 GCGGAGCAGCATACATGTCATAACCGCGGCTGACCGGTGCGGAGCCAAATACAGCTT 891
QY 323 ValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysValTyrGln 342
Db 892 TCCCACTCTGCGGACACACCGTGGCGGTGACGACAGTCTTCTACTGTCTACGAA 951
QY 343 LysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAla 362
Db 952 CAGGAAGACAAAGAGGACACGTTGGCATCACTTGTCCAAAGATCTCATGGCCATCGCC 1011
QY 363 GlyAspAlaLeuLysThrAsnIleThrLeuGlyProMetValLeuProLeuSerGlu 382
Db 1012 GGTGAAGCCCTCAAGGCAAAATCACCACATAGGTGCTTGTGCTTACCGGCGTCAGAA 1071
QY 383 GlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysValLysPro 402
Db 1072 CAACCTCTCTCTCAGCTCCCTAATCGGACGTAATAATCTTCAACCCGAAATGGAAACCA 1131
QY 403 TyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyArgAla 422
Db 1132 TACATACCGGATTTCAAGTGGCCCTCGAACACATTTTGCATTACACGAGGACGAGCG 1191
QY 423 ValLeuAspGluValcIlyLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArg 442
Db 1192 GTGATCGACGACTCCAAAGAATCTACAACTATACAGGACACACGCTTACGAGCTCAAGA 1251
QY 443 MetThrLeuHisArgPheGlyAsnThrSerSerSerSerSerLeuTrpTyrGluMetAlaTyr 462
Db 1252 ATGACACTACATCGTTTGTAAACGCTCATCTTCATCGTTATGTGTACGAGCTTAGCTAC 1311
QY 463 ThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySer 482
Db 1312 ATCGAGCTTAAAGGAGATAGGAGGCGATCGCGTTTGGCAAAATCGCGTTTGGGAGT 1371
QY 483 GlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluLeuMet 502
Db 1372 GGTTCACAGTGAACCTCGCGGTGGAATGTAAACGTCAGATTAAAGACACACCTAAG- 1428
QY 503 ThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProVal 516
Db 1429 ---GAGCGACCATGGTTCGATTGTATCGACCGTTACCGCTGTC 1467

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RESULT 10

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US-09-883-797-11
; Sequence 11, Application US/09883797
; Patent No. US20020066123A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beittemmiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES

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; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/09/883,797
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 08/868,373
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1502
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-883-797-11

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Alignment Scores:
Pred. No.: 1-82e-163 Length: 1502
Score: 1438.50 Matches: 279
Percent Similarity: 74.49% Conservative: 89
Best Local Similarity: 56.48% Mismatches: 113
Query Match: 53.68% Indels: 13
DB: 10 Gaps: 6

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US-09-883-797-2 (1-520) x US-09-883-797-11 (1-1502)

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QY 26 LeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeuHisAsnSer 45
Db 25 ATGCAGAGTTCTCTAGCTCGGTGAAGCTCAAGTACGTGAACACTGGTACCAATATTG 84
QY 46 CysAsnValThrIleLeuPhePheLeuIleLeuProLeuThrGlyThrValLeu 65
Db 85 GTTAAC-----CAATTCTTGAGTTTCTTTTGATC---CCGATCATGGCTATTGTCGCC 135
QY 66 ValGlnLeuThrGlyLeuThrPheAspPheSerGluLeuTrpSerAsnGlnAlaVal 85
Db 136 GTTGAGCTTCTTCGATGGGTGCTGAAGAGATCCTTAATGTTTGAAT-----TCACATC 189
QY 86 GlnLeuAspPheAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeuThrLeu 105
Db 190 CAGTTTGACCTAGTTCAGTTCTATGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 249
QY 106 TyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysProGlu 125
Db 250 TACTTTCATGTCACAGCCAGCCACCATCTACCTCGTTGACTATCTTGTACAAGCCACCT 309
QY 126 AspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPhe 145
Db 310 GTCACGCTGTCGTGC-----CCCTTCGCAACTTTCATGGAACACTCTCGTTGATC 360
QY 146 ThrAspAsp-----ThrValGlnPheGlnArgIleSerAsnArgAlaGlyLeu 162
Db 361 CTCAAGGACCAAGCCTAAGAGCGTCGAGTCCAAATGAGAATCCTTGAACGTTCTGCGCTC 420
QY 163 GlyAspGluThrTyrLeuProArgGlyIleThrSerThrProProLysLeuAsnMetSer 182
Db 421 GGTGAGGAGACTTGTCTCCCTCCGCTATTATTCATTATTCCTCCCAACACCAATGGAC 480
QY 183 GluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLys 202
Db 481 GCGGCTAGAGCGAGGCTCAGATGGTTATCTCGAGGCGCATGGACCATCTTTTCAAGAAA 540
QY 203 ThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnPro 222
Db 541 ACCGGTCTTAAACCTTAAAGACGTCGACATCTTATCGTCAACTGCTCTCTTTCTCTCCC 600
QY 223 ThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSer 242
Db 601 ACACCATCGCTCTCAGCTATGCTCATCAACAAATATAGCTTAGGAGTAAATATCAAGAGC 660
QY 243 TyrAsnLeuGlyGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAsn 262
Db 661 TTCAATCTTTCGGGATGGGTGACGCGGCGCTCATCTCAGTTGATCTAGCCGCGGAC 720
QY 263 LeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeu 282

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Db 721 TTGCTCCAAAGTTTCATCCCAATCAATCAATCATCGTCAGCAGGAGATCATAACGCCT 780
Qy 283 AsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGly 302
Db 781 AATTAATCAAGGCAAGAGAGAGCCATGTTGTTTACCAATATGCTCTCCGCGCATGGT 840
Qy 303 GlyAlaAlaLeuLeuSerAsnArgArgGlnAspArgGlySerIleSerIleSerLeu 322
Db 841 CGCGCAGCCATACATGTCACACCCCGCTGTACCGGTGGCGGCAAAATACAAAGCTT 900
Qy 323 ValAsnValAlaArgThrHisLysGlySerAspAspLysAsnTyrAsnCysValTyrGln 342
Db 901 TCCCAACCTCGTCGGGACACCGTGGCGTACGACCAAGTCTTCTACTGTGTCTACGAA 960
Qy 343 LysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAla 362
Db 961 CAGGAAGCAAAAGAGACAGTGGCATCAACTTGTCCAAAGATCTCATGCCATCGCC 1020
Qy 363 GlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeuProLeuSerGlu 382
Db 1021 GGTGAAGCCCTCAAGGCAAAATCACCACAATAGTCTTGGTCTACCGCGTCAGAA 1080
Qy 383 GlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysValPro 402
Db 1081 CAACTTCTCTCTCCACGTCCTCAATCGGACGTAAATCTTCAACCCGAAATGGAACCA 1140
Qy 403 TyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAla 422
Db 1141 TACATACCGGATTTCAAGCTGGCTTCGAACACTTTTGATTCACGAGGAGGAGAGCG 1200
Qy 423 ValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArg 442
Db 1201 GTGATCGACGAGCTCCAAAGAAATCTACAACATATCAGGAGAACACGTTGAGCGCTCAAGA 1260
Qy 443 MetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTrpTyrGluMetAlaTyr 462
Db 1261 ATGACACTACATCGTTTGGTAACACGTCATCTCATCGTATGTTGAGTACGCTTACGTAC 1320
Qy 463 ThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySer 482
Db 1321 ATCGAGCTTAAGGGAGAAATGAGGAGGAGCGATCGCGCTTGGCAAAATCGCGTTGGGAGT 1380
Qy 483 GlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMet 502
Db 1381 GGTTCACAGTGAACCTCGCGTGTGGAAGTGAACCGTACGATTAAGACACCTAAG--- 1437
Qy 503 ThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProVal 516
Db 1438 ---GACGGACCATGCTCCGATGTTATCGACCGTTACCTGCTC 1476

RESULT 11

US-09-892-325-2
; Sequence 2, Application US/09892325
; Patent No. US20020116735A1
; GENERAL INFORMATION:
; APPLICANT: Kunst et al.
; TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme
; Involved in Very Long Chain Fatty Acid Synthesis
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kiarquist Sparkman Campbell
; Leigh & Whinston, LLP
; STREET: One World Trade Center, Suite
; 1600, 121 S.W. Salmon Street
; CITY: Portland
; STATE: OR
; COUNTRY: USA
; ZIP: 97204-2988
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3.5-inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Word97 & ASCII

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,325
; FILING DATE: 26-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/058,947
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Barp, Ph.D.
; REGISTRATION NUMBER: 41,401
; REFERENCE/DOCKET NUMBER: 5493-50032/DJE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1807
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-892-325-2

Alignment Scores:
Pred. No.: 2,47e-163 Length: 1807
Score: 1438.50 Matches: 279
Percent Similarity: 74.49% Conservative: 89
Best Local Similarity: 56.48% Mismatches: 113
Query Match: 53.68% Indels: 13
DB: 10 Gaps: 6

US-09-883-797-2 (1-520) x US-09-892-325-2 (1-1807)

Qy 26 LeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeuHisAsnSer 45
Db 74 ATGCCAGAGTCTCTAGCTCGGTGAGCTCAAGTACGTGAACCTTGGTTACCAATATTG 133
Qy 46 CysAsnValThrThrIleLeuPheLeuIleLeuLeuProLeuThrGlyThrValLeu 65
Db 134 GTTAAAC-----CATTTCTTGAATTTCTTTTGTATC---CCGATCATGGTATTGTCGCC 184
Qy 66 ValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrpSerAsnGlnAlaVal 85
Db 185 GTTGAGCTCTTCGGATGGTCTCTGAAGAGATCTTAATGTTTGGAAAT-----TCACTC 238
Qy 86 GlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeuThrLeu 105
Db 239 CAGTTTGACCTAGTTTCAGGTTCTATGTTCTCTCTCTTCTTGTCTATCTCATCTCCACTGTT 298
Qy 106 TyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysProGlu 125
Db 299 TACTTCATGTCGAGCCAGCCACCATCTACCTCGTGTGACTATTTCTTTGTTACAGCCACCT 358
Qy 126 AspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPhe 145
Db 359 GTCACGTGTCGTGTC-----CCCTTCGCAACTTTCATGGAACACTCTCGTTGTATC 409
Qy 146 ThrAspAsp-----ThrValGlnPheGlnGlnArgIleSerAsnArgAlaGlyLeu 162
Db 410 CTCAGGACAAGCCTAAGAGCGTCGAGTTCCTCAAAATCAGAAATCCTTGAACGTTCTGCGCTC 469
Qy 163 GlyAspGluThrTyrLeuProArgGlyIleThrSerThrProProLysLeuAsnMetSer 182
Db 470 GGTGAGGAGACTTGTCTCCCTCCCGCTATTCATTATATTCCTCCACACCAACCATGGAC 529
Qy 183 GluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLys 202
Db 530 CGCGCTAGAAGCGGAGGCTCAGATGTTATCTTCGAGGCCATCGAGCATCTTTTCAAGAAA 589
Qy 203 ThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnPro 222
Db 590 ACCGGCTTTAAACCTAAAGACGTCGACATCTTATCGTCAACTGCTCTCTTTCTCTCC 649


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Db 2363 GGTGAGGAGACTTGTCCTCGGCTATTCAATATATTCTCCACACCAACCATGGAC 2422
Qy 183 GluAlaArgAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLys 202
Db 2423 GCGGCTAGAGCGAGCTCAGATGTTATCTTCGAGGCCATGGACGATCTTTTCAAGAAA 2482
Qy 203 ThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnPro 222
Db 2483 ACCGGTCTTAACCTTAAGACGCTGACATCTTATCGTCACTGCTCTCTTTCTCTCCC 2542
Qy 223 ThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleTysSer 242
Db 2543 ACACCATCGCTCTCAGCTATGTCATCAACAATAATAGCTTAGGAGTAATATCAAGAGC 2602
Qy 243 TyrAsnLeuGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAsn 262
Db 2603 TTCAATCTTTCCGGGATGGCTGCAGCGGGCCCTGATCTAGTTGATCTAGCCCGCGAC 2662
Qy 263 LeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeu 282
Db 2663 TTGCTCCAAGTTCATCCCAATCAAAATGCAATCATCGTCAGCAGCAGATCATACGCCT 2722
Qy 283 AsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGly 302
Db 2723 AATTACTATCAAGCAACGAGAGGCCATGTTGTTACCCAATGTCTCTTCGCGCATGGCT 2782
Qy 303 GlyAlaAlaIleLeuSerAsnArgGlnAspArgLysLysSerLysTyrSerLeu 322
Db 2783 GCGCAGCCATACATGTCAAACCGCGGTCGACCGGTGGCGAGCCCAATACAAAGCTT 2842
Qy 323 ValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnValTyrGln 342
Db 2843 TCCACCTCGTCGGACACACCGTGGCGCTGACGACACAGTCTTCTACTGTGTCTACGAA 2902
Qy 343 LysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAla 362
Db 2903 CAGGAAGACAAAGAGGACACAGTGGCATCAACTGTGTCCTCAAGATCTCATGGCCATGCC 2962
Qy 363 GlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeuProLeuSerGlu 382
Db 2963 GGTGAAGCCCTCAAGCAACATCACCACAATAGTCTCTTGGTCTTACCGCGCTCAGAA 3022
Qy 383 GlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysValLysPro 402
Db 3023 CAACTTCTCTCTCAGTCCCTTAATCGGAGCTAAATCTTCAACCGCAATGGAACCA 3082
Qy 403 TyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAla 422
Db 3083 TACATACCGGATTCAAGCTGGCTTCGAACACTTTTGCACTTTCAGCGAGGAGGAGCG 3142
Qy 423 ValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArg 442
Db 3143 GTGATCGAGCGCTCCAAAGAAATCTACAACTATCAGGAGAACACGCTTGAAGCCTCAAGA 3202
Qy 443 MetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTrpTyrGluMetAlaTyr 462
Db 3203 ATGACACTACATCGTTTGGTAACAGTCTCTTCATCGTTATGGTACGAGCTTACTAC 3262
Qy 463 ThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySer 482
Db 3263 ATCGAGTCTAAAGGAGAAATGAGGAGCGGATCGGTTGGCAATCGCGTTGGGAGT 3322
Qy 483 GlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMet 502
Db 3323 GGTTCAGTGAATCTCTCGCTGGGAAATGTAACCGTACGATTAAGACACCTAAG --- 3379
Qy 503 ThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProVal 516
Db 3380 ---GACGAGCATGTCGATTTGATCGACCGTTACCGTGTGC 3418
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RESULT 13

US-09-938-842A-2597

; Sequence 2597, Application US/09938842A

; Patent No. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; FILE REFERENCE: SAME, AND METHODS OF USE

; CURRENT APPLICATION NUMBER: US/09/938,842A

; PRIOR FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 2597

; LENGTH: 1653

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-938-842A-2597

Alignment Scores:

Pred. No.: 2,45e-163 Length: 1653

Score: 1438.00 Matches: 285

Percent Similarity: 68.77% Conservative: 96

Best Local Similarity: 51.44% Mismatches: 123

Query Match: 53.66% Indels: 50

DB: 9 Gaps: 10

US-09-883-797-2 (1-520) x US-09-938-842A-2597 (1-1653)

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Qy 2 AspArgGluArgLeuThrAlaGluMetAlaPheArg----- 13
Db 16 GAGCAAGATCTCTCTCTACCGAGATCGTTAATCGGGATCGAACCATCGGTCCTAAC 75
Qy 14 ---AspSerSerSerAlaValIleArgIleArgArgLeuProAspLeuThrSer 32
Db 76 GCGCGCTCCCAACAGCTCTCGGTAGGTCAGGAGAGGTTGCTGATTTCTTCAGTCG 135
Qy 33 ValLysLeuLysTyrValLysLeuGlyLeuHisAsnSerCysAsnValThrIleLeu 52
Db 136 GTGAACCTGAAGTACGTGAACCTTGTTTACCCTACTACTATAAACCATCGGTT----- 189
Qy 53 PhePheLeuIleLeuProLeuThrGlyThrValLeuValGlnLeuThrGlyLeuThr 72
Db 190 ---TATTTGGGACCATACCG-----GTTCTTGCTGGTGTGTTTAGTGTGAG 234
Qy 73 PheAspThrPheSer-----GluLeuTrpSerAsnGlnAlaValGlnLeuAspThrAla 90
Db 235 GTTGGAGGTTTAAACGAGAGAGAGATTTGG---AAGAAGCTTTGGGACATATGATCTGCA 291
Qy 91 ThrArgLeuThrCysLeuValPheLeuSerPheValLeuThr-----LeuTyrValAla 108
Db 292 ACTGTTATCGCA-----TTCTTCGCTGCTTTGTTTAAACCGCTTGTGTCTACTTCATG 345
Qy 109 AsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysProGluAspGluArg 128
Db 346 TCTGCTCTCGCTCTCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCT 405
Qy 129 LysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPheThrAspAsp 148
Db 406 AAGGTGACAAAGAGAGAGTTCATAGCACTAGCGAATAATCAGGAAAGTTCAGCAAGAGAG 465
Qy 149 ThrValGlnPheGlnArgIleSerAsnArgAlaGlyLeuGlyAspGluThrTyrLeu 168
Db 466 ACATCTCGTTTCAAGAGAGAGATCTTACAAGCCCTCAGGCATAGGCGAGACATACGTC 525
Qy 169 ProArgGlyIleThrSerThrProLysLeuAsnMetSerGluAlaArgAlaGluAla 188
Db 526 CCAAGATCCATCTCTTCATCAGAAAAACATAACAACGATGAAGAAGGTCGTGCAAGGCC 585
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Thu Feb 20 11:03:35 2003

us-09-883-797-2.p2n.rnpb

QY 276 SerThrGluAsnIleThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCys 295
Db 745 AGCAGAGAACATCCTTATACATTTACGCTGGTGATATAAGTCCATGATGTTTCA 804
QY 296 AsnCysIlePheArgMetGlyGlyAlaIleLeuLeuSerAsnArgGlnAspArg 315
Db 805 AATTGCTTTCCTGTTGGTGGCGCGCTATTTTCTCCAAACGCTGGAGATCGT 864
QY 316 LysLysSerLysTyrSerLeuValAsnValValArgThrHisLysGlySerAspLys 335
Db 865 AGACGGTCCCAAGTACGAGTGTACACGGTTCGACCGCATACCGGAGCTGACGACAAG 924
QY 336 AsnTyrAsnCysValTyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAla 355
Db 925 TCCTTTTCGTTGCGTGCAACAAGGAGAGCATGAGAACGCAAAATCGGAGTGGTTGCC 984
QY 356 ArgGluLeuMetSerValAlaGlyAspAlaLeuLysThrAsnIleThrLeuGlyPro 375
Db 985 AAGGACATAACCCGATGTTGCTGTCGAACGGTTAAGAAAAACATAGCAACGTTGGTCCG 1044
QY 376 MetValLeuProLeuSerGluGlnLeuMetPheLeuIleSerLeuValLysArgLysMet 395
Db 1045 TTGATTCCTCCGTTAAGCGAGAACTCTTTTTCGTTACCTTCATGGGCAAGAACTT 1104
QY 396 PheLysLeuLysValLysPro---TyrIleProAspPheLysLeuAlaPheGluHisPhe 414
Db 1105 TTCAAGATAAAATCAAAACATTACTAGCTCCGGATTTCAAACTTGCTATTGACCAITTT 1164
QY 415 CysIleHisAlaGlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLys 434
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QY 435 AspTrpHisMetGluProSerArgMetThrLeuHisArgPheGlyAsnThrSerSerSer 454
Db 1225 CCGATCGATGTAGAGGCATCAAGATCAACGTTACATAGATTGGAAACACTTCATCTAGC 1284
QY 455 SerLeuTrpTyrGluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArg 474
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QY 475 LeuTrpGlnIleAlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeu 494
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QY 495 ArgProValSerThrGluGluMetThrGlyAsnAlaTyrAlaGlySerIleAspGlnTyr 514
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QY 515 ProValLysVal 518
Db 1459 CCGGTCAAATAAT 1470

Search completed: February 19, 2003, 11:45:30
Job time : 160 secs

GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 09:17:27 ; Search time 82 Seconds
(without alignments)
1944.779 Million cell updates/sec

Title: US-09-883-797-2

Perfect score: 2680

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Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-YGAPOP=10 -YGAPEXT=0.5 -DELOB=6 -DELEXT=7

Database :

Issued Patents_NA:*
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2: /cgn2.6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2.6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2.6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2.6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2.6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	1563	58.3	1548	4	US-08-868-373-13
3	1531.5	57.1	1611	4	US-08-868-373-9
4	1519.5	56.7	1783	1	US-08-066-299-11
5	1519.5	56.7	1783	1	US-08-265-047-3
6	1497	55.9	1733	1	US-08-066-299-10
7	1497	55.9	1733	1	US-08-265-047-2
8	1497	55.9	1733	4	US-08-926-522-21
9	1441	53.8	1650	4	US-08-868-373-7
10	1438.5	53.7	1491	4	US-09-058-947A-3
11	1438.5	53.7	1502	4	US-08-868-373-11
12	1438.5	53.7	1807	4	US-09-058-947A-2

13	1438.5	53.7	3722	4	US-09-058-947A-1	Sequence 1, Appli
14	1323.5	49.4	1512	4	US-08-868-373-5	Sequence 5, Appli
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16	1302.5	48.6	1641	4	US-09-362-633-1	Sequence 1, Appli
17	1298	48.4	1479	4	US-08-868-373-3	Sequence 3, Appli
18	383	14.3	383	3	US-08-888-998-3	Sequence 3, Appli
19	383	14.3	383	4	US-09-362-633-3	Sequence 3, Appli
20	171.5	6.4	3680	2	US-08-494-907-1	Sequence 1, Appli
21	171.5	6.4	3680	5	PCT-US96-10986-1	Sequence 1, Appli
22	171.5	6.4	5076	2	US-08-494-907-2	Sequence 2, Appli
23	171.5	6.4	5076	5	PCT-US96-10986-2	Sequence 2, Appli
24	171.5	6.4	6170	2	US-08-494-907-4	Sequence 4, Appli
25	171.5	6.4	6170	5	PCT-US96-10986-4	Sequence 4, Appli
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27	171.5	6.4	6387	5	PCT-US96-10986-3	Sequence 3, Appli
28	171	6.4	7198	4	US-08-994-035C-4	Sequence 4, Appli
29	171	6.4	7198	4	US-09-395-861-4	Sequence 4, Appli
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33	154	5.7	2728	3	US-08-836-402B-7	Sequence 7, Appli
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35	129	4.8	23673	4	US-09-773-816-1	Sequence 1, Appli
36	117.5	4.4	1002	4	US-09-134-001C-1109	Sequence 1109, Ap
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42	114.5	4.3	1485	2	US-08-479-041-23	Sequence 23, Appli
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ALIGNMENTS

RESULT 1
US-08-868-373-1
; Sequence 1, Application US/08868373
; Patent No. 6307128
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Belittenmiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/08/868,373
; CURRENT FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSQ for Windows version 3.0
; SEQ ID NO 1
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-08-868-373-1

Alignment Scores:
Pred. No.: 2,11e-312 Length: 1560
Score: 2680.00 Matches: 520
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-883-797-2 (1-520) x US-08-868-373-1 (1-1560)

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Qy 21 ArgilleArgArgLeuProAspLeuLeuThrSerValLysLysValLysLeu 40
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US-08-868-373-9
; Sequence 9, Application US/08868373
; Patent No. 6307128
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beittemiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/08/868,373
; CURRENT FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1611
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-08-868-373-9
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Score: 1531.50 Matches: 285
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QY 326 ValArgThrHisLysGlySerAspLysAsnTyrAsnCysValTyrGlnLysGluAsp 345
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QY 346 GluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAlaGlyAspAla 365
Db 1030 GAAATAACAAGGTAGGTGTTCCCTTATCAAGGATCTGATGCGAGTTCGCGGTGAAGCC 1089
QY 366 LeuLysThrAsnIleThrThrLeuGlyProMetValLeuProLeuSerGluGlnLeuMet 385
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QY 386 PheLeuIleSerLeuValLysArgLysMetPheLysLeu--LysValLysProTyrIle 404
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QY 405 ProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyArgAlaValLeu 424
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QY 425 AspGluValGlnLysAsnLeuAspLysAspTyrPHisMetGluProSerArgMetThr 444
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QY 485 LysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluLysMetThrGly 504
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QY 505 AsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal 518
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RESULT 5

US-08-265-047-3
; Sequence 3, Application US/08265047
; Patent No. 5679881
; GENERAL INFORMATION:

; APPLICANT: Metz, James G.
; APPLICANT: Lardizabal, Kathryn D.
; APPLICANT: Lassner, Michael
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding a Plant Cytoplasmic Protein
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,047
; FILING DATE: 23-JUN-94
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/160,602
; FILING DATE: 30-NOV-93
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/796,256
; FILING DATE: 20-NOV-91

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/933,411
; FILING DATE: 21-AUG-92

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/066,299
; FILING DATE: 20-MAY-93

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09863
; FILING DATE: 13-NOV-92

; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen

; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer

; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler

; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE 101-1

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1783 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: double
; TOPOLOGY: linear

; MOLECULE TYPE: cDNA to mRNA

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1030	GAAGTAAACAAGGTAGGTGGTTCCTATCCRAAGGATCTGATGGCAGTTGCCGGTGAAGCC	1089
366	LeuIysThrAsnIleThrThrLeuGlyProMetValLeuProLeuSerGluGlnLeuMet	385
1090	CTAAAGGCCAACATCACGACCGCTTGGTCCCTCGTCTCCCATGTTCAGAACAACTCCCTC	1149
386	PheLeuIleSerLeuValLysArgLysMetPheLysLeu--LysValLysProTyrIle	404
1150	TTCTTTGCCCATCTAGTGGCAGTAAAGTCTCAAGATGACGAACGTGAAGCATACATC	1209
405	ProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAlaValLeu	424
1210	CCAGATTCAAGTTGGCAGCAACCTTCTGCATCCATGCAAGAGGCAAGCAGTGTG	1269
425	AspGluValGlnLysAsnLeuAspLeuLysAspTyrPheHisMetGluProSerArgMetThr	444
1270	GATGAGCTCGAGACCAACTTGAGGTTGACGCCATGGCACCTTGAACCCCTCGAGGATGACA	1329
445	LeuHisArgPheGlyAsnThrSerSerSerSerLeuTyrTyrGluMetAlaTyrThrGlu	464
1330	CTGTATAGTTTGGGAACACATCGAGTAGCTCATTTATGTTACGAGTGGCATACGCTGAA	1389
465	AlaLysGlyArgValLysAlaGlyAspArgLeuTyrGlnIleAlaPheGlySerGlyPhe	484
1390	GCAAAGGGAGGATCCGTAAAGGTGATCGAACTTGGATGATTTGGTTGGTTCAGGTTTC	1449
485	LysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMetThrGly	504
1450	AAAGTAAACAGTGTGTGTGGAGGGCTTTGAGGAGTGTCAATCCGGCTAGAC--GAGAAG	1506
505	AsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal	518
1507	AATCCTTGGATGATGAATTTGAGAAATTCCTTCCTGTCATGTG	1548

RESULT 6

US-08-066-299-10

; Sequence 10, Application US/08066299

; Patent No. 5445947

; GENERAL INFORMATION:

; APPLICANT: James George Metz

; APPLICANT: Kathryn Dennis Lardizabal

; APPLICANT: Michael W. Lassner

; TITLE OF INVENTION: Fatty Acyl CoA: Fatty Alcohol

; TITLE OF INVENTION: O-Acyltransferases

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Calgene, Inc.

; STREET: 1920 Fifth Street

; CITY: Davis

; STATE: CA

; COUNTRY: USA

; ZIP: 95616

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh 6.0.7

; SOFTWARE: Microsoft Word 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/066,299

; FILING DATE: 19930520

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/796,256

; FILING DATE: 20-NOVEMBER-1991

; APPLICATION NUMBER: 07/933,411

; FILING DATE: 21-AUGUST-1992

; APPLICATION NUMBER: PCT/US92/09863

; FILING DATE: 13-NOVEMBER-1992

US-08-265-047-3

Alignment Scores:
 Pred. No.: 1,24e-172 Length: 1783
 Score: 1519,50 Matches: 284
 Percent Similarity: 75,30% Conservative: 88
 Best Local Similarity: 57,49% Mismatches: 115
 Query Match: 56,70% Indels: 7
 DB: 1 Gaps: 4

US-09-883-797-2 (1-520) x US-08-265-047-3 (1-1783)

QY	26	LeuProAspLeuLeuThrSerVallylsLeuLysTyrVallylsLeuLysGlyLeuHisAsnSer	45
Db	85	CTCCCAACTCAAGTCCTCCCAACTTACACACGTCGAAGTCGGCTACCAC-----	138
QY	46	CysAsnValThrThrIleLeuPhePheLeuIleIleLeuProLeuThrGlyThrValLeu	65
Db	139	---TACTTAATCTCCAATGCCCTCTCTCGTATTATCATCCCTCTTTGGCGCTGCCTCG	195
QY	66	ValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTyrSerAsnGlnAlaVal	85
Db	196	GCACCACTCTCCCTCTCTCGGCCCATGACTTGTCCCTGCTCTTC-----GACCTCCTT	249
QY	86	GlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeuThrLeu	105
Db	250	CGCGCAACCTCTCCCGCTTCGTTGTTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	309
QY	106	TyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysProGlu	125
Db	310	CATTCTTGACCCGGCGCTAGGAATGTCTACTTGGTGGACTTTCCTGCTGCTATAAGCCTCAC	369
QY	126	AspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPhe	145
Db	370	CGGAACCTGTATACATCCACGAGATGTTTCATGGACCGGACCTCCCGGCGCGGTTCGTTT	429
QY	146	ThrAspAspThrValGlnPheGlnGlnArgIleSerAsnArgAlaGlyLeuGlyAspGlu	165
Db	430	TCTAAGGAGAATATTGAGTTTCAGAGGAAGATCTTGGAGAGGCGCGGTATGGCGCGGAA	489
QY	166	ThrTyrLeuProArgGlyIleThrSerThrProProLysLeuAsnMetSerGluAlaArg	185
Db	490	ACCTACGTCCCGCAATCCGTCACTAAGTTCGCGCGCGCGAGCATAGCAGCACCAGG	549
QY	186	AlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLysThrGlyIle	205
Db	550	CGCGAGGCGGAGGAGTGATGTACGGGGCGATCGACGAGGTGTGGAGAAGACGGGGGTG	609
QY	206	LysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnProThrProSer	225
Db	610	AAGCCGAAGCAGATAGAGAACTACTGTGGTGAACATGCAGCTTGTTTAACCAACGCGCTCG	669
QY	226	LeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSerTyrAsnLeu	245
Db	670	CTGTCATCATGATAGTTAACCATTAACAAGCTTAGGGGTAATATCTAGCTATAATCTT	729
QY	246	GlyGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAsnLeuLeuLys	265
Db	730	GTTGGCATGGGTTCAGTGTGGGCTCATTTCCATTGTAICTTGCCCAAGACCTCCTACAG	789
QY	266	AlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsnTrpTyr	285
Db	790	GTTTACCCTAACACATATGTGTTAGTAGTGAGCACAGAAACATGACCTTAATTTGGTAC	849
QY	286	PheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGlyAlaAla	305
Db	850	TGGGCAATACCGCTCATCAACCACTGCGCTATTTTCGATGGGTGGCGGTGCC	909
QY	306	IleLeuLeuSerAsnArgArgGlnAspArgLysLysSerLysTyrSerLeuValAsnVal	325
Db	910	ATCATCCTCTCAACCCGTGGCGTGATCGTCGCGCATCAAGTACCAACTCCTTTCACACA	969
QY	326	ValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysValTyrGlnLysGluAsp	345

```

: ATTORNEY/AGENT INFORMATION:
:
: NAME: Elizabeth Lassen
: REGISTRATION NUMBER: 31,811
: NAME: Donna E. Scherer
: REGISTRATION NUMBER: 34,111
: REFERENCE/DOCKET NUMBER:
:
: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: (916) 753-6313
: TELEFAX: (916) 753-1510
: INFORMATION FOR SEQ ID NO: 1
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 1733 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
:
: MOLECULE TYPE: cdna to mRNA
:
: US-08-066-299-10

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Alignment Scores:			
Pred. No.:	6.05e-170	Length:	1733
Score:	1497.00	Matches:	282
Percent Similarity:	74.75%	Conservative:	88
Best local Similarity:	56.97%	Mismatches:	117
Query Match:	5.86%	Indels:	8
DB:	1	Gaps:	5
US-09-883-797-2 (1-520) x US-08-066-299-10 (1-1733)			

Qy	26	LeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeuHisAsnSer	45
		::: :: ::: :: ::	
Db	120	CTCCCAACTTCAGTCTCATCACTTACACCACGTCAAGCTCGGCTACCA	179

QY	46	CysAsnValThrThrIleLeuPhePheLeuIleIleLeuProLeuThrGlyThrValLeu	65
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		:::	
Db	174	---TACTTAATCTCCAATGCCCTCTPCTCGATTATCATCCCCCTTTGGGCTCGGTTCG	230

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345 CAITTTCTGTGACCGCGCCAGGAATGCTCTACTTGGTGGACTTTGGATGCTATAAGCCTCAA 404

QY 126 AspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPhe 145

Dbp 405 CCGAACCTGATACATCCACGAGATGTTTCATGGACGGACCTCCCGGCCGCTGTTT 464

QY 146 ThrAspAspThrValGlnPheGlnGlnArgGileSerAsnArgAlaGlyLeuGlyAspGlu 165

465 TCTAAGGAGAATATTGAGTTTCAGAGGAAGATCTTCGAGAGGCCGGTATGGTTCGGGA 524
.....
Db

166 ThrTyrLeuProArgGlyIleThrSerThrProProLysLeuAsnMetSerGluAlaArg 185
.....
QY

525 ACCATATGTCCTCCGCAATCCGGTCACTAAGGTGCCCGGAGCCGAGCATAGCAGCAGCCAGG 584 db

186 AlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGlnIlyvsThrGlyTle 205 Dy

dbb
585 GCCGAGGCGGAGGAGTGATGTACGGGGCGATCGACGAGGTGTTGGAGAAGACGGGGGTG 644

dbb 645 AAGCCGAAGCAGATACGAACTACTGGTGGTGANCTGCAGCTGTTTAACCCCAAGCCGTCG 704

245 LeuseiAraMetIIleValAShIShtyLysMetArgGluAspIleLysSerTyraSnLeu
 250
 705 CTGTCATCCATGATAGTTAAACCATTACAAGCTNAGGGGTAATATACTTAGCTATAATCTT 764

246 GlyGlyMetClyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAsnLeuLeuLys 265

[illegible]

RESULT 7

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US-08-265-047-2
; Sequence 2, Application US/08265047
; Patent NO. 5679881
; GENERAL INFORMATION:
;
; APPLICANT: Metz, James G.
; APPLICANT: Lardizabal, Kathryn D.
; APPLICANT: Lassner, Michael
; TITLE OF INVENTION: Nucleic Acid
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:

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[illegible]

Qy 483 GlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMet 502
 Db 1381 GGTTCAGTGTAACTCTGCGGTGGAGTGTAAACGTCACGATTAAAGACACCTAAG--- 1437
 Qy 503 ThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProVal 516
 Db 1438 ---GACGGACCATGGTCGGATTGTATCGACCGTTACCCCTGTC 1476

RESULT 12

US-09-058-947A-2

; Sequence 2, Application US/09058947A

; Patent No. 6274790

; GENERAL INFORMATION:

; APPLICANT: Kunst et al.

; TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme

; TITLE OF INVENTION: Involved In Very Long Chain Fatty Acid Synthesis

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klarquist Sparkman Campbell

; ADDRESSEE: Leigh & Whinston, LLP

; STREET: One World Trade Center, Suite

; CITY: Portland

; STATE: OR

; COUNTRY: USA

; ZIP: 97204-2988

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Disk, 3.5-inch

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows NT

; SOFTWARE: Word97 & ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/058,947A

; FILING DATE:

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/043,831

; FILING DATE: April 14, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: David J. Earp, Ph.D.

; REGISTRATION NUMBER: 41,401

; REFERENCE/DOCKET NUMBER: 5493-50032/DJE

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (503) 226-7391

; TELEFAX: (503) 228-9446

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1807

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

US-09-058-947A-2

Alignment Scores:

Pred. No.:

Score: 7,14e-163

Percent Similarity: 1438/50

Best Local Similarity: 74.49%

Query Match: 56.48%

DB: 113

Matches: 13

Indels: 13

Gaps: 6

US-09-883-797-2 (1-520) x US-09-058-947A-2 (1-1807)

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Db 74 ATGCCAGAGTTCCTAGTCTCGGTGAGCTCAAGTACGTGAACTTGGTTACCAATATTG 133

Qy 46 CysAsnValThrIleLeuPhePheLeuIleLeuProLeuThrGlyThrValLeu 65

Db 134 GTTAAC-----CATTTCTTGAGTTTCTTTTGTATC---CCGATCATGCTATTGTCGCC 184

Qy 66 ValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrpSerAsnGlnAlaVal 85

Db 185 GTTCAGCTCTCTCGATGGGTCCCTGAAGAGATCCCTAATAGTTTGAAT-----TCACATC 238
 Qy 86 GlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeuThrLeu 105
 Db 239 CAGTTTGACCTAGTTCAGGTTCTATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 298
 Qy 106 TyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysProGlu 125
 Db 299 TACTTCATGTCCAAAGCCACGACCATCTACCTGTTGACTATCTTCTGTATACAGCCACCT 358
 Qy 126 AspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPhe 145
 Db 359 GTCACGTGTCGTGTC-----CCCTTCGCAACTTTCATGGAACACTCTCGTTTGATC 409
 Qy 146 ThrAspAsp-----ThrValGlnPheGlnArgIleSerAsnArgAlaGlyLeu 162
 Db 410 CTCAAGGACCAAGCCTAAGAGCGTCAGATGGTTATCTTCGAGGCCATGGACGATCTTTCAAGAA 469
 Qy 163 GlyAspGluThrTyrLeuProArgGlyIleThrSerThrProProLysLeuAsnMetSer 182
 Db 470 GGTGAGGAGACTTGTCTCCCTCCGCTATTCATTATATTCCTCCACACCAACCATGGAC 529
 Qy 183 GluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLys 202
 Db 530 GCGGCTAGAGCGAGGCTCAGATGGTTATCTTCGAGGCCATGGACGATCTTTCAAGAA 589
 Qy 203 ThrGlyLeuLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnPro 222
 Db 590 ACCGGTCTTAACCTAAGACGTCGACATCTTATCGTCAACTCTCTCTCTCTCTCTCTCT 649
 Qy 223 ThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSer 242
 Db 650 ACACCATCGCTCTCAGCTATGGTCAACAATAATAGCTAGGAGTATATATCAAGAC 709
 Qy 243 TyrAsnLeuGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAsn 262
 Db 710 TTCATCTTTCGGGATGGGCTGACGCGGGCTGATCTCAGTTGATCTAGCCCGGAC 769
 Qy 263 LeuLeuLysAlaAsnProAsnSerTyrAlaValValValSerThrGluAsnIleThrLeu 282
 Db 770 TTGCTCCAAGTTCATCCCAATCAATGCAATCATCGTCAGCAGGAGATCATACCCCT 829
 Qy 283 AsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGly 302
 Db 830 AATTACTATCAAGGCAAGGAGAGCCATGTTGTTACCCCAATTTCTCTCTCCGATGGGT 889
 Qy 303 GlyAlaAlaIleLeuLeuSerAsnArgArgGlnAspArgLysSerLysTyrSerLeu 322
 Db 890 GCGCAGCCATACATGTCAAACCGCCGCTGACCGGTGCGGCGGCGGCAAAATACAAGCTT 949
 Qy 323 ValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysValTyrGln 342
 Db 950 TCCACCTCGTCCGACACACCGTGGCGGTGACGACAACTCTTCTACTGTGTCTACGAA 1009
 Qy 343 LysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAla 362
 Db 1010 CAGGAAGACAAAGAGGACACGTGGCATCAACTTGTCCAAAGATCTCATGCCCATCGCC 1069
 Qy 363 GlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeuProLeuSerGlu 382
 Db 1070 GGTGAAGCCCTCAAGGCAAAACATCACCACATAGTCTTGTCTCTCCCGCGGTACAGAA 1129
 Qy 383 GlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysValLysPro 402
 Db 1130 CACTTCT 1189
 Qy 403 TyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyClyArgAla 422
 Db 1190 TACATACCGGATTCAGAGTGGCCCTTCGACACTTTTGCATTCACGAGGAGGACGAGCG 1249
 Qy 423 ValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArg 442

Db 3023 CAACCTCTCTCTCCTCACGTCCTCAATCGGACGTAAATCTTCAACCCGAAATGGAAACCA 3082
Qy 403 TyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyAlaGlyAla 422
Db 3083 TACATACCGGATTTTCAAGCTGGCTTCGAACACTTTTGCATTCACGAGGAGCAGAGCG 3142
Qy 423 ValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArg 442
Db 3143 GTGATCGAGAGCTCCAAAGAAATCTACAACATATCAGAGAACACGTTGGAGCCCTCAAGA 3202
Qy 443 MetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTrpTrpGluMetAlaTyr 462
Db 3203 ATGACATACATCGTTTGGTAACACGTCATCTTCATCGTTATGGTACGAGCTTAGCTAC 3262
Qy 463 ThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySer 482
Db 3263 ATCGAGTCTAAAGGAGAAATCAGGAGAGCGCATCCGCTTTGGCAAAATCGGTTTGGGAGT 3322
Qy 483 GlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMet 502
Db 3323 GGTTTCAAGTGTAACTCTGCGGTGTGGAATGTAAACCTACGATTAAAGACACCTTAAG --- 3379
Qy 503 ThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProVal 516
Db 3380 --GACGGACCATGGTCCGATTGTATCGACCGTTACCCTGTC 3418

RESULT 14
US-08-868-373-5
; Sequence 5, Application US/08868373
; Patent No. 6307128
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beitlenmiller, Martha A.
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/08/868, 373
; CURRENT FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-08-868-373-5

Alignment Scores:
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Score: 1323.50 Matches: 254
Percent Similarity: 70.83% Conservative: 86
Best Local Similarity: 52.92% Mismatches: 129
Query Match: 49.38% Indels: 11
DB: 4 Gaps: 4

US-09-883-797-2 (1-520) x US-08-868-373-5 (1-1512)

Qy 47 AsnValThrThrIleLeuPhePheLeuIleLeuProLeuThrGlyThrValLeuVal 66
Db 76 AAATTAAGATGGTTTCTTCAAGATCTCTTATCTTAAATGGCAGGATAGCCATG 135
Qy 67 GlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrpSerAsnGlnAlaValGln 86
Db 136 AAAGGATCTAAGATCAACGTAGAGATCTCCAAAG---TCTCCCTCCACCACATACAG 192
Qy 87 LeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeuThrLeuTyr 106
Db 193 AACAACTCCAAACCATAGCCCTCTATTGTTCTTGTCTGTTTGTGGATCCCTCTAC 252
Qy 107 ValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysProGluAsp 126
Db 253 ATGTTAACCCCGACCTAAACCCCGTTACCTTGTGTGTTTCTCTCTGCTACCTTCCACCGTCG 312

Qy 127 GluArgLysIleSerValAspSerPheLeu-----ThrMetThrGluGluAsnGly 143
Db 313 CATCTCAAGGTCAGTATCCAAACCTAATGGACACGCAAGACGTCGCAAGACAGACAGCGC 372
Qy 144 -----SerPheThrAspThrValGlnPheGlnGlnArgIleSerAsn 158
Db 373 ATGTGTTGGAAGAACAAAGAGAGAGGACCATTTAGTTGACTTCCAGGAGAAGATTTCTTGA 432
Qy 159 ArgAlaGlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProProLys 178
Db 433 CGTTCGGTCTTGTGTCAAGAAACCTACATCCCGAGGTCCTTCAGTCTTCCACCTTCAG 492
Qy 179 LeuAsnMetSerGluAlaArgAlaGluAlaValMetPheGlyAlaLeuAspSer 198
Db 493 CAAGGCGATGGTCTTCCACGTAAAGAGACGGAAGAAGTAATCTTCGGAGCTCTTGACAAT 552
Qy 199 LeuPheGluLysThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSer 218
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Qy 219 LeuPheAsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGlu 238
Db 613 ACGTTTAAATCCAACTCCATCCATCCCTCCATGATTGTGAACAAGTACAACTCAGAGAC 672
Qy 239 AspIleLysSerTyrAsnLeuGlyGlyMetGlyCysSerAlaGlyLeuIleSerIleAsp 258
Db 673 AACATCAAGAGTTTGAATCTTGGAGGATGGGTTCAGTGCAGTTCAGTCTTATAGCTGTGAT 732
Qy 259 LeuAlaAsnAsnLeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGlu 278
Db 733 GTCGCTAAGGGATTACTACAAGTTTCATAGGAACACTTATGCTATTGTAGTAGACACAGAG 792
Qy 279 AsnIleThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIle 298
Db 793 AACATCAGTCAAGAACTTATCTTGGGAAAAAACAATCAATGCTAGTACAACTGTTTG 852
Qy 299 PheArgMetGlyGlyAlaIleLeuLeuSerAsnArgGlnAspArgLysLysSer 318
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Qy 319 LysTyrSerLeuValAsnValAlaArgThrHisLysGlySerAspAspLysAsnTyrAsn 338
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Qy 339 CysValTyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeu 358
Db 973 TGTGCGACACAAGAGAGGATGAAGATGTTAATTTGGAGTTACCTTTGACAAAGAAATCTA 1032
Qy 359 MetSerValAlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeu 378
Db 1033 CCTATGGTGGTGCAGAGGACTCTTAAGATAAATATCCCAACTTTGGTCTCTTGTACTT 1092
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Db 1093 CCATTAAAGAGAGAGCTAGCCCTTCTTATTACTTTTGTCAAGAAGAAGTATTTCAAGCCA 1152
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Db 1273 GAGCGTCAAGAATGACACTACACAGGTTTGGTAACACTTCTTCTAGCTCAATCTGGTAC 1332
Qy 459 GluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIle 478
Db 1333 GAGTTACGTTATACAGAAGCTAAAGAGGATGAAGGAAGAGATAGGATTTGGCAGATT 1392
Qy 479 AlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSer 498


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QY 415 CysIleHisAlaGlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLys 434
Db |||||||
QY 1165 TGTATTTCATGCGGAGGAGCCGTCGATCGTAGCTAGAGAAGAACTTAGGACTATCG 1224
Db |||||||
QY 435 AspTrpHisMetGluProSerArgMetThrLeuHisArgPheGlyAsnThrSerSer 454
Db |||||||
QY 1225 CCGATCGATGTGGAGGCATCTAGATCAACGTTACATAGATTTGGGAATACTTCATCTAGC 1284
Db |||||||
QY 455 SerLeuTrpTyrGluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArg 474
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QY 1285 TCAATTGGTATGTAATTAGCATACATAGAGGCAAGGCAAGCAATGAAGAAAGGAATAAA 1344
Db |||||||
QY 475 LeuTrpGlnIleAlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeu 494
Db |||||||
QY 1345 GCTTGGCAGATTGCTTTAGGATCAGGGTTAAGTGTAAATAGTCCGTTGGTGGCTCTA 1404
Db |||||||
QY 495 ArgProValSerThrGluGluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyr 514
Db |||||||
QY 1405 CGCAATGTCAAGGCATCG-----CCAAATAGTCCTTGGCAACATTGCATCGATAGATAT 1458
Db |||||||
QY 515 ProValLysVal 518
Db |||||||
QY 1459 CCGGTTAAATTT 1470
Db |||||||
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Search completed: February 19, 2003, 10:53:40
Job time : 110 secs

GenCore version 5.1.4_p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 09:12:57 : Search time 1710 Seconds
(without alignments)
4924.943 Million cell updates/sec

Title: US-09-883-797-2
Perfect score: 2680
Sequence: 1 MDRERLTAEMAFROSSAVI.....EMTGNWAGSIDQYPKVQVQ 520

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool/US09883797/runat_14022003_102501_19515/app_query.fasta_1.711
-DB=EST -OPMT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09883797@cgn_1_1_2874_@runat_14022003_102501_19515 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_est1: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_nam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rod: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1505	56.2	1981	11	AY109713	AY109713 Zea mays
2	1092	40.7	1496	11	AY108343	AY108343 Zea mays
3	1031	38.5	735	12	BG599761	BG599761 EST504656
4	1024	38.2	800	12	BG646966	BG646966 EST508585
5	1006.5	37.6	867	13	BI949576	BI949576 HVSME1001
6	997	37.2	840	10	BE055710	BE055710 GA_Ea003
7	996.5	37.2	915	14	BQ510080	BQ510080 EST617495
8	987.5	36.8	958	12	BG444087	BG444087 GA_Ea002
9	970.5	36.2	864	12	BG444393	BG444393 GA_Ea002
10	960	35.8	663	14	BQ405604	BQ405604 GA_Ed008
11	939	35.0	671	13	BQ281418	BQ281418 BJ281418
12	939	35.0	765	14	BQ989474	BQ989474 QGF17M08
13	937.5	35.0	754	13	BM112516	BM112516 EST560052
14	928	34.6	755	14	BQ872186	BQ872186 QG113006
15	927	34.5	738	12	BG586676	BG586676 EST488444
16	925	34.5	684	9	AL505481	AL505481 AL505481
17	923	34.4	722	14	BU012426	BU012426 QGJ1008.Y
18	906.5	33.8	680	14	BQ407349	BQ407349 GA_Ed010
19	906	33.8	770	14	BQ855453	BQ855453 QGB26K03
20	905	33.8	814	17	BH664493	BH664493 BOMPA49TF
21	905	33.8	634	14	BQ245540	BQ245540 TaEI5023D
22	890	33.2	642	13	BQ302152	BQ302152 BJ302152
23	887	33.1	715	12	BG128306	BG128306 EST473952
24	887	33.1	830	10	BE642615	BE642615 Cr12.6.11
25	886	33.1	753	12	BG123587	BG123587 EST469233
26	883.5	33.0	699	9	AJ497664	AJ497664 AJ497664
27	883	32.9	715	14	BQ931166	BQ931166 QGF27M06
28	880	32.8	715	17	BH685156	BH685156 BOMMW34TF
29	879	32.8	821	17	BH693376	BH693376 BOHUS43TR
30	878.5	32.8	692	14	BQ403143	BQ403143 GA_Ed005
31	874.5	32.6	912	12	BG837722	BG837722 Zm10.05C0
32	869	32.4	629	14	BQ801648	BQ801648 WHE2816_H
33	869	32.4	685	12	BG443505	BG443505 GA_Ea002
34	868.5	32.4	750	17	BH490415	BH490415 BOCBR78TF
35	867	32.4	717	12	BG124000	BG124000 EST469646
36	863	32.2	705	12	BG626005	BG626005 HVSMEa001
37	861	32.1	693	12	BG441374	BG441374 GA_Ea001
38	859	32.1	612	14	Z26005	Z26005 ATTS1282.Gr
39	859	32.1	745	12	BG128875	BG128875 EST474521
40	858.5	32.0	661	14	BQ148102	BQ148102 NF058602F
41	855	31.9	675	12	BF635850	BF635850 NF040G12D
42	854.5	31.9	669	14	BQ407360	BQ407360 GA_Ed010
43	845	31.5	602	12	BF255395	BF255395 HVSMEf000
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1981)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.


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DEFINITION Zea mays PC0065510 mRNA sequence.
ACCESSION AY108343
VERSION AY108343.1 GI:212111421
HTC.
SOURCE Zea mays.
ORGANISM Zea mays
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
  clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1496)
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
  Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of
  Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1496)
AUTHORS Coe,E.C.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
  Missouri, Columbia, MO 65211, USA
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      /note="this sequence is part of a project of EST
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      Mapping Project"
BASE COUNT 277 a 455 c 503 g 261 t
ORIGIN

Alignment Scores:
Pred. No.: 2,33e-123 Length: 1496
Score: 1092.00 Matches: 213
Percent Similarity: 72.39% Conservatived: 57
Best Local Similarity: 57.10% Mismatches: 84
Query Match: 40.75% Indels: 19
DB: 11 Gaps: 3

US-09-883-797-2 (1-520) x AY108343 (1-1496)
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|||||:|||||:|||||:|||||:|:|
Db 1486 GGCAGCAGTCGTACATGCCGCGCTGCTTGCAGCCCAACGCCAGCTGCGCCACCATG 1427
::: |||||:|||||:|||||:|||||:|||||:|
QY 182 SerGluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGlu 201
::: |||||:|||||:|||||:|||||:|||||:|
Db 1426 AAGGATGGCGCGCCGACAGCGTCCAGCGCCATGTCGCGCGGTGGAGAGCTGTTCCAG 1367
LysThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsn 221
||| |||:|||||:|||||:|||||:|||||:|
Db 1366 AAGTGC CGCGTCCGGCCCAAGGACGTGGCGTCTGGTGTCAACTGCAGCCTCTTCAAC 1307
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QY 222 ProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLys 241
|||||:|||||:|||||:|||||:|||||:|
Db 1306 CCGAGCGCCCTCCTGTCCGCCATGATPCTCAACCATACAAAGATGCGCGCAACATCCTG 1247
SerTyrAsnLeuGlyGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsn 261
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Db 1246 AGCTACAACCTGGGGGCATGGCTGCACGCGCGCTATCGCCATCGACCTGGCCCGC 1187
AsnLeuLeuLysAlaAsn-ProAsnSerTyrAlaValValValSerThrGluAsnIleTh 281
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Db 1186 GACATGCTCCAGGCCCGCGCGCTGGCCTGGCGGTGGTGGTCCAGCAGGAGCGCGTCTC 1127
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||||| ||| |||||:|||||:|

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QY	445	LeuHisArgPheGlyAsnThrSerSerLeuTyrTyrGluMetAlaTyrThrGlu	464
Db	664	CTTCATCATGATTGGCAACACATTCAGACGCTCCCTTTGGTACGAATTGGCTATTGGAA	723
QY	465	AlaLysGlyArg	468
Db	724	GCCCAAGGTAGG	735
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LOCUS	BG646966	800 bp	linear
DEFINITION	EST508585 HOGA Medicago truncatula cDNA clone phOGA-15E18 5' end,		
ACCESSION	BG646966		
VERSION	BG646966.1	GI:13782078	
KEYWORDS	EST.		
SOURCE	barrel medic.		
ORGANISM	Medicago truncatula		
REFERENCE	1 (bases 1 to 800)		
AUTHORS	Hahn,M.G., Ojanen-Reuhs,T., Samac,D., Town,C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.		
TITLE	ESTs from roots of Medicago truncatula treated with oligogalacturonides of DP 6-20		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Michael G. Hahn Complex Carbohydrate Research Center University of Georgia 220 Riverbend Road, Athens, GA 30602-4712, USA Tel: 706-542-4457 Fax: 706-542-4412 Email: hahn@ccrc.uga.edu G390572e TIGR sequence name: MTMBT33TK More information is available at: www.medicago.org Seq primer: SKmod (CTA gAA CTA gTg gAT CC).		
FEATURES	Location/Qualifiers		
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	/cultivar="Al7"		
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	/clone="phOGA-15E18"		
	/clone_lib="HOGA"		
	/tissue_type="3 day old seedling roots"		
	/dev_stage="24 hours after treatment in the dark at 26 C with 0.5 mg/ml oligogalacturonides (DP 6-20) in the presence of 100 ug/ml Gentamicin"		
	/lab_host="XtOLR"		
	/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOLR cells."		
BASE COUNT	242 a	157 c	177 g
ORIGIN	224 t		
Alignment Scores:	2,09e-115	Length:	800
Pred. No.:	1024.00	Matches:	193
Score:	88.64%	Conservative:	41
Percent Similarity:	88.64%	Mismatches:	29
Best Local Similarity:	73.11%	Indels:	2
Query Match:	38.21%	Gaps:	0
DB:	12		
US-09-883-797-2	(1-520) x	BG646966	(1-800)
QY	176	ProProLysLeuAsn-MetSerGluAlaArgAlaGluAlaValMetPheGlyAl	195
Db	11	CCACCTAAATCCATGTATGGCTGAAGCAAGCAAGCTGAAGAGGTATGTTGGTGC	70

QY 195 aleuAspSerLeuPheGluLysThrGlyIleLysProAlaGluValGlyIleLeuIleVa 215
 Db 71 TATTGATGAGGTCTCTCAAAAACCTGGTGAAGGCTAAGATATTGGGATTTTGGTTGT 130
 QY 215 lasnCysSerLeuPheAsnProThrProSerLeuSerAlaMetIleValAsnHistyrlly 235
 Db 131 GAATTGTAGTTGTTTAAATCCAAACCATCTCTTCTGCGCATGATTGTGAATCATATAA 190
 QY 235 smetArgGluAspIleLysSerTyAsnLeuGlyGlyMetGlyCyssSerAlaGlyLeuII 255
 Db 191 GTTGAGAGAAATATCTTTCAGTTATAATCTTGGTGGTATGGTGTAGTGGTCTTAT 250
 QY 255 eSerIleAspLeuAlaAsnAsnLeuLysAlaAsnProAsnSerTyAlaValValVa 275
 Db 251 CTCATTGACCTTGCCAAACACCTCTACAGGTACATCAAACTCATATGCGCTTAGTAGT 310
 QY 275 lserThrGluAsnIleThrLeuAsnTrpTyPheGlyAsnAspArgSerMetLeuLeuCy 295
 Db 311 GAGCATGGAGAACATAACACTAAACTGCTATTTCGGCAACGACACATCAATCTAGTGCC 370
 QY 295 sasnCysIlePheArgMetGlyGlyAlaAlaIleLeuLeuSerAsnArgArgGlnAspAr 315
 Db 371 AAATGTCTCTTTAGATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 430
 QY 315 gLysLysSerLysTySerLeuValAsnValValArgThrHisLysGlySerAspAspLy 335
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 QY 335 sasTyAsnCysValTyGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAl 355
 Db 491 ATCTAGCGGTCTCTTTCAAGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 550
 QY 355 aArgGluLeuMetSerValAlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyPr 375
 Db 551 AAAAGACCTAATGGCTGTGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 610
 QY 375 oMetValLeuProLeuSerGluGlnLeuMetPheLeuIleSerLeuLysArgLysMe 395
 Db 611 ATTAGTCTACCTATGTCGAACAGCTCTTATTTCGGGACATTTGGTGGCGGAAATAT 670
 QY 395 tPheLysLeuLysValLysProTyrlleProAspPheLysLeuAlaPheGluHisPheCy 415
 Db 671 CTTCAAGATGAATAAATCAACATACATCTCTGATTTTAAATAGCTTTTGAGCATTTTG 730
 QY 415 sIleHisAlaGlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAs 435
 Db 731 TATTTCATGCTGTGTGAAGAGGCTGTTTGGATGAGTTGGAGAA-AATCTTGATTTAAGTGA 789
 QY 435 pTrpHisMet 438
 Db 790 TTGGCATATG 799

RESULT 5
 B1949576
 LOCUS
 DEFINITION
 HVSME10014L13f Hordeum vulgare spike EST library HVCDA0012
 (Fusarium infected) Hordeum vulgare cDNA clone HVSME10014L13f, mRNA
 sequence.
 B1949576
 VERSION
 B1949576.1 GI:16290960
 KEYWORDS
 EST.
 SOURCE
 Hordeum vulgare.
 ORGANISM
 Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Hordeum.
 REFERENCE
 1 (bases 1 to 867)
 AUTHORS
 Wing, R., Muehlbauer, G.J., Close, T.J., Klein, H., Wise, R., Heinen,
 S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T.,
 Simmons, J., Fenton, R.D., Malatrasi, M., Choi, D.W., Oates, R. and Main,
 D.
 TITLE
 Development of a genetically and physically anchored EST resource

JOURNAL
COMMENT

for barley genomics: Fusarium infected Morex spike cDNA library
 Unpublished (2001)
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Total hq bases = 555
 Seq primer: AATTAACTCTACATAAGGG
 High quality sequence stop: 610.
 Location/Qualifiers
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 /db_xref="taxon:4513"
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 (Fusarium infected)"
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 /note="Vector: pBluescript SK(-); Site1: EcoRI; Site2: XhoI; Plants were grown at the University of Minnesota in the GJ Muehlbauer lab; spikes were harvested and snap frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium graminearum inoculation (Heinen). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders. Also see Close TJ, Wing R, Klein, H., Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)."

FEATURES
source

BASE COUNT 200 a 223 c 260 g 182 t 2 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.48e-113 Length: 867
 Score: 1006.50 Matches: 199
 Percent Similarity: 86.27% Conservative: 46
 Best Local Similarity: 70.07% Mismatches: 39
 Query Match: 37.56% Indels: 5
 DB: 13 Gaps: 0
 US-09-883-797-2 (1-520) x B1949576 (1-867)
 QY 220 PheAsnProThrProSerLeuSerAlaMetIleValAsnHistyrllyMetArgGluAsp 239
 Db 2 TTCAACCCGAGCCGCTACTGTCGCCATGGTGGTGAACATTACAGCTGAGAGGGAAC 61
 QY 240 IleLysSerTyAsnLeuGlyGlyMetGlyCyssSerAlaGlyLeuIleAspLeu 259
 Db 62 ATAATCAGCTACATCTGGGAGGAATGGGGTGCAGTCCGGGCTCTTGTCCATAGATCTG 121
 QY 260 AlaAsnAsnLeuLysAlaAsnProAsnSerTyAlaValValSerThrGluAsn 279
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BASE COUNT      250 a      209 c      190 g      215 t
ORIGIN

Alignment Scores:
Pred. No.:      9,78e-109      Length:      864
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Percent Similarity:      88.70%      Conservative:      38
Best Local Similarity:      72.80%      Mismatches:      26
Query Match:      36.21%      Indels:      1
DB:      12      Gaps:      1

US-09-883-797-2 (1-520) x BQ444393 (1-864)

Qy 278 GluAsnIleThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCys 297
Db 3 GAGAACATTACTCTCAACTGGGACTTCGGCAACGACCGATCCATGCTACTCTCAACTGC 62
Qy 298 IlePheArgMetGlyGlyAlaAlaIleLeuLeuSerAsnArgGlnAspArgLysLys 317
Db 63 TTGTTCGGTATGGCGGGTCCCGCGATCTTCTATCAAAACCGGTCTATCCGCGCGCG 122
Qy 318 SerLysTyrSerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyr 337
Db 123 TCCAAGTACCAACTCATCCACACCGTACGAAACCCACAAGAGCGCCAGCACAAATGCTAC 182
Qy 338 AsnCysValTyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGlu 357
Db 183 AACTGCGCTTCCCAACGTTGAGCAGACACCAACAAATAGGCGTTTCCCTCTCCAAAGAC 242
Qy 358 LeuMetSerValAlaGlyAspAlaLeuLysThrAsnIleThrLeuGlyProMetVal 377
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Db 303 CTCGCCATGTCGGAACAACTCTCTTTTTCATCACTTTAGTACCCGAAAGCTCTCAA 362
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Qy 458 TyrGluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGln 477
Db 543 TACGAACCTAGCTTACTCGGAAGCCAAAGGAAGGATCCGAAAGGTGATCGGACATGGCAG 602
Qy 478 IleAlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProVal 497
Db 603 ATTGCATTGGGTCAGGGTTTAATCAACAGCTGCTGTATGGAAGCATTTGAAGACCAT 662
Qy 498 SerThrGluGluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProVal 516
Db 663 AATCCAGCAAG---GAGAGAGTCCATGGATTGATGAATGAATGATATGCGCTGTT 716

RESULT 10
BQ405604
LOCUS
DEFINITION
GA_Ed0084G03f Gossypium arboreum 7-10 dpa fiber library Gossypium
ARBOREUM cDNA clone GA_Ed0084G03f, mRNA sequence.
ACCESSION
BQ405604
VERSION
BQ405604.1
GT:21093291
KEYWORDS
EST.
SOURCE
Gossypium arboreum.
ORGANISM
Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

```

```

Rosidae; eurousids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 663)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total High Quality bases = 559
Seq primer: TAATACGACTCACTATAGG
High quality sequence stop: 652.
FEATURES
Location/Qualifiers
1..663
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/strain="AKA"
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/clone="GA_Ed0084G03f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/notes="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT      186 a      169 c      150 g      157 t      1 others
ORIGIN

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Alignment Scores:
Pred. No.:      1.25e-107      Length:      663
Score:          960.00      Matches:      169
Percent Similarity:      91.82%      Conservative:      33
Best Local Similarity:      76.82%      Mismatches:      18
Query Match:      35.82%      Indels:      0
DB:      14      Gaps:      0

US-09-883-797-2 (1-520) x BQ405604 (1-663)

Qy 278 GluAsnIleThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCys 297
Db 2 GAGAACATTACTCTCAACTGGTACTTCGGCAACGACCGATCTATGCTCTCAAAATGC 61
Qy 298 IlePheArgMetGlyGlyAlaAlaIleLeuLeuSerAsnArgGlnAspArgLysLys 317
Db 62 CTCCTCCGATGGGGGTGCGCAATCTCTCTCCAAACCGCTCATCCGATCGCACCGC 121
Qy 318 SerLysTyrSerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyr 337
Db 122 TCCAATACCAACTCATTCACACCGTACGACGACACAAAGTGCAGATGACAAATGCTAC 181
Qy 338 AsnCysValTyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGlu 357
Db 182 AACTCGCTCTCCAGGTGAGGAGCAGACCAAAAGATCGCATTTCCCTCTCGAAAGAC 241
Qy 358 LeuMetSerValAlaGlyAspAlaLeuLysThrAsnIleThrLeuGlyProMetVal 377
Db 242 CTCATGGGTGTCGCGGAGAGCCCTTAAACCAACATCACCACTCTGGGCGCACATGTT 301
Qy 378 LeuProLeuSerGluGlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLys 397
Db 302 CTCCTCCATGTCGAGCAACTCTCTGTTTTCGTCACCTGTTGGCAAGAAAGTGTGAAG 361
Qy 398 LeuLysValLysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHis 417
Db 362 ATGAAGATCAAAACCTATATCCAGATTTCAAGTTCGATTCGCAACATTTTTCATCAT 421
Qy 418 AlaGlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLysAspTrpHis 437
Db 422 GCAGGTGGGAGCGGTGCTAGATGAGCTTGAAGAAACCTTGACCTTACAGATTGGCAC 481

```

unpublished (2002).
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA

Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@atgc.org [michelmorerevegmail.ucdavis.edu]
 belongs to contig Qc_CA_Contig4873, see http://cgdb.ucdavis.edu/
 for details.
 Plate: OGF17 row: M column: 08.

FEATURES

Location/Qualifiers
 1..765
 /organism="Lactuca sativa"
 /cultivar="L.serriola"
 /db_xref="taxon:4236"
 /clone="OGF17M08"
 /lab_host="E.coli"
 /note="Vector: pBRCDNA5fiAB: The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and size bias. Details of each source of RNA and library construction can be obtained at http://cgdb.ucdavis.edu/
 TAG_LIB=OG_EFGHJ lettuce serriola
 TAG_TISSUE=flowers pre-fertilized
 TAG_SEQ=GCCTGACGGG"
 219 a 182 c 163 g 201 t

BASE COUNT
 ORIGIN

Alignment Scores:

Pred. No.: 6,25e-105 Length: 765
 Score: 939.00 Matches: 167
 Percent Similarity: 86.96% Conservative: 53
 Best Local Similarity: 66.01% Mismatches: 33
 Query Match: 35.04% Indels: 0
 DB: 14 Gaps: 0

US-09-883-797-2 (1-520) x BQ989474 (1-765)

QY 187 GluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLysThrGlyLys 206
 DB 4 GAGCGGACGAGTTATGATACGGAGCTTTAGATAATCTTTCCACGCGGAGTAAA 63
 QY 207 ProAlaGluValGlyLeuLeuValAsnCysSerLeuPheAsnProThrProSerLeu 226
 DB 64 CCAAAAGACATCGGCATCCTGTGGTGAACGTGTAGCTGTTCATCGACTCCTCTTC 123
 QY 227 SerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSerTyrAsnLeuGly 246
 DB 124 TCTTCATGATCGTTAACAAATACAAATTAAGAGGTAACATCGCGGAGCTTCAATTTGGGC 183
 QY 247 GlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAsnLeuLysAla 266
 DB 184 GGAATGGATGACGCGCGGTGTGATGTCATCGATCTGGCCAAAGATATGTACAGTT 243
 QY 267 AsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsnTrpTyrPhe 286
 DB 244 CACCGGAATACATACGCGCTGTTGTGACGACCGAAACATCACCCAAAATTGGTATTC 303
 QY 287 GlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGlyGlyAlaAla 306
 DB 304 GGAACAAAAGTCCATGATGCCCAATTTGTTATTCGAGTCGGTGTCTCGAGTT 363
 QY 307 LeuLeuSerAsnArgGlnAspArgLysLysSerLysTyrSerLeuValAsnValVal 326
 DB 364 TTACTCTCCAAACAAATCAATCGATAAAGACGACGAAAATACAACTCGTTATGCGTG 423
 QY 327 ArgThrHisLysGlySerAspAspLysAsnTyrAsnCysValTyrGlnLysGluAspGlu 346
 DB 424 AGAACCCACCGGGTGCAGATGAGAAAGCTTTCGCTGCTATATCAAGAACAGACGCC 483
 QY 347 ArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAlaGlyAspAlaLeu 366

Db 484 GCCGGAACAACTGCTCTCTTTATCAAAAGATCTCATGCAATCGCGGCGCACTG 543
 QY 367 LysThrAsnIleThrThrLeuGlyProMetValLeuSerGluGlnLeuMetPhe 386
 Db 544 AAAACCAACATCACTACTCTGGGCCACTTGTCTTCCAACTAGTGAACAGCTCTTTTC 603
 QY 387 LeuIleSerLeuValLysArgLysMetPheLysValLysLysProTyrIleProAsp 406
 Db 604 TTCTGCATTTAATAATAAAAAATCTTCAATAACAACATCAAAACCTACATCTCTGAT 663
 QY 407 PheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAlaValLeuAspGlu 426
 Db 664 TTCAAAATAGCTTTCGACCATTTCTGCATCCACCTGGTGTGCGGCTGTGATTGATGAG 723
 QY 427 ValGlnLysAsnLeuAspLeuLysAspTrpHisMetGlu 439
 Db 724 CTTGAGAAGAATCTGCAGCTATATACCCGACACATGTTGNA 762

RESULT 13
 BM112516 754 bp mRNA linear EST 26-NOV-2001
 LOCUS EST560052 potato roots Solanum tuberosum cDNA clone cPR014F19 5'
 DEFINITION end, mRNA sequence.
 ACCESSION BM112516
 VERSION BM112516.1 GI:17075564
 KEYWORDS EST.
 SOURCE potato.
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 1 (bases 1 to 754)
 van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Van Aken,S.,
 Utterback,T., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C.,
 Tanksley,S. and Baker,B.
 Generation of ESTs from potato roots
 Unpublished (2001)
 Contact: Research Genetics, Libraries Division
 Tel: 1-800-711-6195
 Email: cdna@resgen.com
 For clone info: please contact Research Genetics, Libraries
 Division tel 1-800-711-6195, email cdna@resgen.com
 Seq primer: 73

FEATURES
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 1..754
 /organism="Solanum tuberosum"
 /cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="cPR014F19"
 /clone_lib="potato roots"
 /tissue_type="roots"
 /dev_stage="in vitro grown stem cuttings"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
 XhoI; supplier: Cornell University Tanksley lab;
 sequencing: The Institute for Genomic Research. Roots were
 isolated from in vitro grown stem cuttings on CM medium.
 Roots were isolated two weeks after placing the stem
 cuttings from in vitro grown plants on medium."
 245 a 124 c 155 g 230 t

BASE COUNT
 ORIGIN

Alignment Scores:
 Pred. No.: 9.36e-105 Length: 754
 Score: 937.50 Matches: 168
 Percent Similarity: 87.70% Conservative: 26
 Best Local Similarity: 77.05% Mismatches: 30
 Query Match: 34.98% Indels: 3
 DB: 13 Gaps: 0

US-09-883-797-2 (1-520) x BM112516 (1-754)

QY 87 LeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeuThrLeuTyr 106

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Db 19 ATTACACTTCAACCGGTCTAACCAGTTGATAGTGTATTTTCTACTAGGGGTGTAT 78
Qy 107 ValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysProGluAsp 126
Db 79 TA-TGTAAAAAACCTAGACCGGTTTATTGTTGATTTTGCATGTTTCAAAACCGAAGAA 137
Qy 127 GluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPheThr 146
Db 138 GAACGAAAAATATCTCGATTCTGTTTGAATATGACAGAGAAATGGTGGCTTGA 197
Qy 147 AspAspThrValGlnPheGlnArgIleSerAsnArgAlaGlyLeuGlyAspGluThr 166
Db 198 GACGAACATATAGTATTTCAAAAAAGATATCTCATCGTCTGTTTAGTGACGAGACG 257
Qy 167 TyrLeuProArgGlyIleThrSerThrProLysLysLeuAsnMetSerGluAlaArgAla 186
Db 258 TATTTGCCATAAGGATCATCATCCCAACCAACCTCAACATCAAGAGAGACGACGTGCT 317
Qy 187 GluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLysThrGlyIleLys 206
Db 318 GAGCGGAGCGGTTATGTTGGTGCATGGATTGATTATTTAGTAAACACAAATCAAG 377
Qy 207 ProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnProThrProSerLeu 226
Db 378 CCAGAGAAATTTGGAATCTTTTAGTGAATTTAGTGTGTTTAAATCCCAACGCGCATCGT 437
Qy 227 SerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSerTyrAsnLeuGly 246
Db 438 TCATCAATGATTTGCAATCACTACAAAGCTCAAACTGACATCAAAAGTTATAATTAGT 497
Qy 247 GlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnLeuLysAla 266
Db 498 GGAATGGGATGATGCTGGCTTAATTTCAATTTGATTTAGCCAAACAACTATTAAAGCA 557
Qy 267 AsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsnTrpTyrPhe 286
Db 558 AATCAAAATTCATATGCTGTTGTTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTATTT 617
Qy 287 GlyAsnAspArgSerMetLeuLeuCysAsnGlyIlePheArgMetGlyGlyAlaIle 306
Db 618 GGAATGATGATGATCAATGTTGCTATGCAATTTGATTTATTCGATGGGAGGAGCGCAAG 677
Qy 307 LeuLeuSerAsnArgAlaAspArgLysLysSerLysTyrSerLeuValAsnValVal 326
Db 678 CTTTGTCTACAAGTCGAA-GATCGACC-CGGTCTAATATGAGTTGCTTACACCGGTT 735
Qy 327 ArgThrHisLys 330
Db 736 CGAACCCATAAG 747

RESULT 14
BQ872186
LOCUS
DEFINITION
QGI13006.yg.ab1 QG-ABCDI lettuce salinas Lactuca sativa cDNA clone
QGI13006, mRNA sequence.
ACCESSION
BQ872186
VERSION
BQ872186.1 GI:22258744
KEYWORDS
EST.
SOURCE
Lactuca sativa.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Lactuceae; Lactuceae;
Lactuca.
1 (bases 1 to 755)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison
P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)

```

```

COMMENT
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig4873, see http://cgdb.ucdavis.edu/
for details.
Plate: QGI13 row: 0 column: 06.
Location/Qualifiers
FEATURES
source
1..755
/organism="Lactuca sativa"
/cultivar="Salinas"
/db_xref="taxon:4236"
/clone="QG13006"
/clone_lib="QG-ABCDI lettuce salinas"
/lab_host="E.Coll"
/note="vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_LIB=QG-ABCDI
TAG_TISSUE=roots
TAG_SEQ=GTTCACGGG"
BASE COUNT 217 a 181 c 156 g 201 t
ORIGIN
Alignment Scores:
Pred. No.: 1.4e-103 Length: 755
Score: 928.00 Matches: 165
Percent Similarity: 86.85% Conservative: 53
Best Local Similarity: 65.74% Mismatches: 33
Query Match: 34.63% Indels: 0
DB: 14 Gaps: 0
US-09-883-797-2 (1-520) x BQ872186 (1-755)
Qy 187 GluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLysThrGlyIleLys 206
Db 3 GAGCGGAGCAGCGTTATGTACGAGCTTTAGATAAATCTGTTTCCAGTACCGAGTTAAA 62
Qy 207 ProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnProThrProSerLeu 226
Db 63 CCAAAAGACATCGGCATCCTTGTGGTGAACCTGTAGCTGTTCATCCGACCTCTCCTTG 122
Qy 227 SerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSerTyrAsnLeuGly 246
Db 123 TCTTCCATGATCGTTAAACAAATACAAATTAAGAGGTAAACATCCGAGCTTCAATTTGGGC 182
Qy 247 GlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnLeuLysAla 266
Db 183 GGAATGGGATGACGCGCGGTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 242
Qy 267 AsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsnTrpTyrPhe 286
Db 243 CACCGGAATACATACCCGCTGCTGTGTGTCAGCACCCGAAACATCACCCAAATTTGTTTC 302
Qy 287 GlyAsnAspArgSerMetLeuLeuCysAsnGlyIlePheArgMetGlyGlyAlaIle 306
Db 303 GGAACAAAAAGTCCATGCTGATCCCAATTTGTTTATTCGAGTCGGTGGTTCGAGTT 362
Qy 307 LeuLeuSerAsnArgArgGlnAspArgLysLysSerLysTyrSerLeuValAsnValVal 326
Db 363 TTACTCTCAACAAATCAATCGATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 422
Qy 327 ArgThrHisLysGlySerAspAspLysAsnTyrAsnCysValTyrGlnLysGluAspGlu 346

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Db 423 AGAACCCACCGTGGTGCAGATGAGAAAGCTTTCGGTTCGTTATATCAAGAACAGACGCC 482
QY 347 ArgGlyThrIleGlyValSerLeuAlaArgGluMetSerValAlaGlyAspAlaLeu 366
Db 483 GCCGGAAGAACTGGTGCTTTATCAAAAGATCTCATGGCAATCGCGGCGGCACTG 542
QY 367 LysThrAsnIleThrThrLeuGlyProMetValLeuProLeuSerGluGlnLeuMetPhe 386
Db 543 AAAACCAACATCACTACTCTGGGCCACTTGTCTCCAAATCACTGAGCACTCTCTTC 602
QY 387 LeuIleSerLeuValLysArgLysMetPheLysLeuLysValLysProTyrIleProAsp 406
Db 603 TTCTGCACCTTAAATAATAAAATCTTCAATAAACACATCAAAACCTACATTCCTGAT 662
QY 407 PheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAlaValLeuAspGlu 426
Db 663 TTCAATAGCTTTCACCATTTCTGCATCCACGCTGGTGGTGGGCTGTGATTGATGAG 722
QY 427 ValGlnLysAsnLeuAspLeuLysAspTrpHis 437
Db 723 CTTGAAAGATCTGCAGCTATACCCGACACAT 755

RESULT 15
BG586676
LOCUS
DEFINITION
EST488444 MHAM Medicago truncatula/Glomus versiforme mixed EST
library cDNA clone pMHAM-44017 5' end, mRNA sequence.
ACCESSION
BG586676
VERSION
BG586676.1 GI:13601740
KEYWORDS
EST.
SOURCE
Medicago truncatula/Glomus versiforme mixed EST library.
Medicago truncatula/Glomus versiforme mixed EST library.
Eukaryota; mixed EST libraries.
1 (bases 1 to 738)
Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J.
and Fraser,C.M.
TITILE
ESTs from roots of Medicago truncatula after colonization with
Glomus versiforme, 2001
JOURNAL
Unpublished (2001)
COMMENT
Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
Email: mjharrison@noble.org
Noble EST name: N385742e TIGR sequence name: MTD093TK More
information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gTg gAT CC).
FEATURES
Location/Qualifiers
1..738
/organism="Medicago truncatula/Glomus versiforme mixed EST
library"
/cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="pMHAM-44017"
/clone.lib="MHAM"
/tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XL0LR"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-zap phage using Ex-assist
helper phage and propagated in XL0LR cells."
200 a 97 c 185 g 256 t
BASE COUNT
ORIGIN

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Alignment Scores:

Pred. No.:	1-79e-103	Length:	738
Score:	927.00	Matches:	169
Percent Similarity:	84.62%	Conservative:	40
Best local Similarity:	68.42%	Mismatches:	36
Query Match:	12	Indels:	2
DB:	12	Gaps:	1

US-09-883-797-2 (1-520) x BG586676 (1-738)

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Db 3 TATGCTGTGTGTGTAGTACTGAGAATAATTAACCAAAATGGTATTTGGTAATAAGAAA 62
QY 291 SerMetLeuLeuCysAsnCysIlePheArgMetGlyGlyAlaAlaIleLeuLeuSerAsn 310
Db 63 TCTATGTTGATCCGAATTTGTTTCGCTGGTGGTGGCGCGGTTCTGCCTTCGAAC 122
QY 311 ArgArgGlnAspArgLysLysSerLysTyrSerLeuValAsnValValArgThrHisLys 330
Db 123 AAAGGCTGTGATAGAGAGGAGGCTAAGTATAGCTTGTTCATCTGTGTGAGGACTATAA 182
QY 331 GlySerAspAspLysAsnTyrAsnCysValTyrGlnLysGluAspGluArgGlyThrIle 350
Db 183 GGTGCTGATGATAAAGCAATTTAAGTGTGTTTATCAAGAACAAGACCATGTTGGAAACT 242
QY 351 GlyValSerLeuAlaArgGluLeuMetSerValAlaGlyAspAlaLeuLysThrAsnIle 370
Db 243 GGTGTGCTTGTCTAAAGATCTTATGGCTATTGCTGGTGGTCTTAAAGACGAATATA 302
QY 371 ThrThrLeuGlyProMetValLeuProLeuSerGluGlnLeuMetPheLeuIleSerLeu 390
Db 303 ACACTTTGGGTCCTCTTGTGTACTGTGTAGTGAACAGCTTTGTTTTTACTACTTTG 362
QY 391 VallysArgLysMetPheLysLeuLysValLysProTyrIleProAspPheLysLeuAla 410
Db 363 GTTATTAAAGAAATGGTTTAAATCCAAAACCTAAGCCTTATATACCTGATTTTAAAGCTGCT 422
QY 411 PheGluHisPheCysIleHisAlaGlyGlyArgAlaValLeuAspGluValGlnLysAsn 430
Db 423 TTTGAGCATTTTGTATTTATTCATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 482
QY 431 LeuAspLeuLysAspTrpHisMetGluProSerArgMetThrLeuHisArgPheGlyAsn 450
Db 483 TTGACGCTTATGCTGATCATGTTGAGGCATCTAGAATGACCTTGCATAGATTTGCAAT 542
QY 451 ThrSerSerSerSerLeuTrpTyrGluMetAlaTyrThrGluAlaLysGlyArgValLys 470
Db 543 ACTTCTTCAAGTTCAATTTGCTATCAATTGCTTACATTAAGCTTAAAGAGGATGAGA 602
QY 471 AlaGlyAspArgLeuTrpGlnIleAlaPheGlySerGlyPheLysCysAsnSerAlaVal 490
Db 603 AAGGAAACAGAAATTTGGCAGATTCATTTTGGGAGTGGTGGTGGTGGTGGTGGTGGTGGT 662
QY 491 TrpLysAlaLeuArgProValSerThrGluMetThrGlyAsnAlaTrpAlaGlySer 510
Db 663 TGCAGGCTATGAACACATGTGAAGCTTCAACCTATG-----AGTCCATGGGAAGATTGC 716
QY 511 IleAspGlnTyrProValLys 517
Db 717 ATTGATAGGTATCCAGTTGAG 737

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Search completed: February 19, 2003, 10:51:51
Job time : 1724 secs

